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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:07:09; Search time 22.5 Seconds (without alignments) 100.734 Million cell updates/sec Run on:

AUDET-909-1 52

1 eevvpAgmsys 11 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL Database :

sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp archeap:*

SUMMARIES

		Description	O98fx1 rhizobium	O8rq86 fusobacteri	074056 cenarchaeum	Q9ury8 schizosacch	O8r126 mus musculu	O8vd18 mus musculu	040129 lycopersico	09xvk4 caenorhabdi	043733 homo sapien	Q9bha5 plasmodium	09bh83 plasmodium	001487 rattus norv	Q9pdm6 xylella fas	014122 homo sapien	Q12479 saccharomyc	0971s2 sulfolobús
		ID	Q98FX1	Q8RG86	074056	Q9URY8	Q8R126	Q8VD18	Q40129	Q9XVK4	043733	Q9BHA5	Q9BH83	Q01487	O9PDM6	014122	Q12479	097182
		DB	16	16	П	m	11	11	10	2	4	2	Ŋ	11	16	4	m	17
		Match Length DB	387	1063	3472	840	471	484	225	425	556	583	583	670	749	1902	156	219
₩	Query	Match	73.1	73.1	73.1	71.2	69.2	69.2	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	65.4	65.4
		Score	38	38	38	37	36	36	35	35	35	35	35	32	35	32	34	34
	Result	No.	7		ო	4	ហ	φ	7	80	თ	10	11	12	13	14	15	16

4 24 4	O9fn14 arabidopsis O9x0u3 thermotoga O9v914 drosophila O96cs0 homo sapien O9dzys mus musculu Q8r8k6 thermoanaer O96mb2 homo sapien
028342 096MU1 098MD6 098BP5 098BP5 098BP5 098TX6 096914 02833 080TX62 090X04 02833 080TX62 090X04 02833 090X04 090X04 090X04 090X04 090X04 090X06 000X06 000X06 000X06 000X06 000X06 000X06 000X06 000X06 000X06 000	Q9FNL4 Q9x0U3 Q9V914 Q96CS0 Q9D2X9 QBRBK6
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10 14 11 16 4
2552 2607 2707	333 343 347 347 35 35 35 35 35 35 35 35 35 35 35 35 35
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44444444000000000000000000000000000000	
1111 73333333333555555555555555555555555	W 4 4 4 4 4 4 9 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0

ALIGNMENTS

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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hippurate hydrolase.
MiR3583.
Rhizobium loti (Mesorhizobium loti).
Rationium loti (Mesorhizobium subdivision, Rhizobiaceae group, Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 7:331_338(2000).

EMBL; AP003002; BAB50445.1; -.

InterPro; IPR002933; Peptidase M20.

Pfam; PF01546; Peptidase M20; Ī.

Hydrolase; Complete protecome.

SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
                                      387 AA
                                     PRT;
                                   PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                  NCBI_TaxID=381;
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                                   Q98FX1
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RESULT 1
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367 DEAIPHGMSY 376

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J. Bacteriol. 180:5003-5009(1998).
-!- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOWAINS).
EMBL; AF083072; AAC62699.1; -.
InterPro; IPRO0015; BPD transp.
InterPro; IPRO001680; WD40.
Ffam; PF00400; WD40; 4.
SMART; SM00320; WD40; 2.
PROSITE; PS00402; BPD TRANSP_INN_MEMBR; UNKNOWN_1.
Hypothetical protein; Repeat: WD repeat.
SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
                                                                                                                            Gaps
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Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                                                                                                                                                                                                            73.1%; Score 38; DB 16; Length 1063; 60.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.1%; Score 38; DB 1; Length 3472; 54.5%; Pred. No. 1e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                1; Indels
                                             01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  PRT; 3472 AA
                  PRT; 1063 AA
                                                                                  Fusobacterium nucleatum (subsp. nucleatum).
                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                          Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                       Cenarchaeum symbiosum.
Archaea; Crenarchaeota; Cenarchaeum.
                                     Created)
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Hypothetical 367.1 kDa protein.
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Best Local Similarity 54.5.
Best Local Similarity 6.5.5.
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Best Local Similarity 60...
6; Conservative
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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195 EIVPNGLNYS 204
                                     01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                  2 EVVPXGMSYS 11
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=46770;
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                             Q8RG86;
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                   Q8RG86
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074056
RESULT 2
         Q8RG86
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                      STRAIN=972H-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Bubmitch (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Ali32779; CABGOUS-11, -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS, Ilate_transp.
Pfam; PF0916; Sulfate_transp; 1.
TIGRFAMS; TIGR00815; Sulfate_transp; 1.
SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%; Score 37; DB 3; Length 840; 77.8%; Pred. No. 37; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC025810; AAH25810.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NÖN TER 1 1 1
SEQÜENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              087126;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 54.5 kDa protein (Fragment).
                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 AA.
                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
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                                        PRT;
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Best Local Similarity 60.07
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Best Local Similarity 77.8%
Thea 7; Conservative
                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                          Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
                                                                                                                                                                              SPAC869.05C.
                                                               Q9URY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8R126
                                          Q9URY8
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Q8R126
RESULT 4
                     Q9URY8
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RESULT 6

Q8VD18

1 EEVVPXGMSYS 11

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AW536441

Q8VD18;

08VD18

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.3%; Score 35; DB 4; Length 556; Best Local Similarity 66.7%; Pred. No. 64; Matches 1; Indels Matches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 48; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    EMBL, 281109; CAB03241.1; ...
InterPro; IPR000719; Euk_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD0000001; Euk_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 556 AA; 59059 MW; ECB00E4033FB2528 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BHA5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 50.0
nes 5; Conservative
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244 VVPAGLTYS 252
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                                                                       R10D12.10. Caenorhabditis elegans
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                                                        R10D12.10 protein.
                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                 NCBI_TaxID=6239;
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Matches
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.2 kba protein precursor.
Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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"Nature and regulation of pistil-expressed genes in tomato.";
Plant Mol. Biol. 28:691-711(1995).
BMBL, U20592, AAB0497.1;
InterPro; IPR002160; Kunitz_legume.
Pfam, PF00197; Kunitz_legume; 1.
ProDom, PD000991; Kunitz_legume; 1.
SMART; SM00452; SII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; DB 10; Length 225; 54.5%; Pred. No. 24; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                        69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 33; tive 2; Mismatches 2; Indels
                                      01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637; AAH17637.1; -.
MGD; MGI:2138595; AW536441.
SEQUENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 225 UNKNOWN.
225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00283, SÓYBEAN KUNITZ, UNKNOWN 1.
Hypothetical protein, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 AA.
     484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-VF36; TISSUE-PISTIL;
MEDLINE-95375233; PubMed=7647301;
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 DEVVPNGKTYA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 EVIPAGASYN 248
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                   Mus musculus (Mouse)
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RESULT 7 Q40129

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Gaps

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Q9XVK4 Q9XVK4;

RESULT 8 **Q9XVK4**

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670 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PDM6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09PDM6
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
DNA-binding protein AT-BP2 (ALPHA1-antitrypsin promoter binding protein 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
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0
                                                                                                            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                   Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;
Plasmodium fallciparum choline transporter (PfSCT1) gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AX007372; AAK14816.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEQUENCE FROM N.A.

Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;

Plassmodium falciparum choline transporter (PfSCT1) gene.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AY007374; AAK14818.1; --

EMBL; AY007373; AAK14817.1; --

EMBL; AY0071373; AAY14817.1; --

EMBL; AY0071373; AAY14817.1; --

EMBL; AY0071374; AAY14817.1; --

EMBL; AY0071375; AAY14817.1; --

EMBL; AY0071375; AAY14817.1; --

EMBL; AY007137; AAY147.1; --

                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67; 1:ve 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                        EMBL, AY007375; AAG17947.1; -
InterPro, IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SEQUENCE S83 AA; 66917 MW; 2B2BFAE3E395E049 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 IIPVGLSYS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 IIPVGLSYS 235
                                                                                   Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCT1.
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSYS 11
                            Choline transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choline transporter.
                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                         NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BH83;
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09BH83
AC 09BH8
AC 09BH8
DT 01-JU
DT 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Araya J.B., Bove J.M., Briones M.R.S., Barros M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Calauco M.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Coutinho L.L., Cristofani M., Dias.Neto E., Docena C., El-Dorry H., Farga J.S., Franca M.C.A., Ferrola M., Furlan L.R., Adanica M., Fraga D.S., Franco M.C., Frohme M., Furlan L.R., Adanica M.J., Goldman M.H., S., Gomes S.L., Kitajima J.P., N. Krieger J.B., Hobelsel J.D., Junqueira M.L., Kamper B.L., Kitajima J.P., M. Krieger J.B., Kuramae E.B., Ladgret F., Lambais M.R., Leite L.C.C., Lemos B.G.M., Madeira A.M.B.N., Madeira H.M.F., Martino C.L., Martino E.M.F., Martino C.L., Martins E.M.F., Matsukuma A.Y.,
                                                              Mitchelmore C., Traboni C., Cortese R.;
Mitchelmore C., Traboni C., Cortese R.;
"Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-antitrypsin promoter and to the major histocompatibility. Complex class I enhancer."

Nucleic Acids Res. 19:141-147(1991)

-- FUNCTION: BINDS TO THE ALPHA1-ANTITRYPSIN PROMOTER, TO THE KAPPA IMMUNGLOBULIN GENE ENHANCER, AND TO THE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I ENHANCER, AND TO THE MAJOR HISTOCOMPATIBILITY REGULATOR CONCENTING THE ALPHA1-ANTITRYPSIN EXPRESSION IT MAY ACT AS A NEGATIVE REGULATOR BY INTERPERING AT THE ALPHA1-ANTITRYPSIN PROMOTOR WITH ANOTHER NUCLEAR PROTEIN, CALLED LF-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: HIGHLY SIMILAR TO AT-BP1 AND TO THE PRDII-BF1 FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 2.
SMART; SM00355; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS0157; ZNC_FINGER_C2H2_2; 2.
Zinc-finger; Nuclear protein, DNA-binding; Transcription regulation; Metal-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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0
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-!- MISCELLANEOUS: ACIDIC AMINO ACID REGION MAY BE INVOLVED IN TRANSCRIPTIONAL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.3%; Score 35; DB 11; Length 670; 66.7%; Pred. No. 78; 1:ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDD2324152590C17 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C(2)H(2) CLASS.
C(2)H(2) CLASS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC-FINGERS.
STRAIN=SPRAGUE-DAWLEY; TISSUE=THYROID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=9A5C;
MEDLINE=20365717; PubMed=10910347;
                                 MEDLINE=91187610; PubMed=1901405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X54250; CAA38151.1; -. HSSP; P15822; 1BBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 WPAGLTYS 384
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156 AA

PRELIMINARY;

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RESULT 15

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Menck C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.A., Pereira G.A.G., Pereira H.A., Jr., Perguero J.B.,
Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A de Rosa V.E. Jr., da S.Iva A.M., da Silva M.A. Jr.,
A da Silva A.C.R., da Silva A.M., da Silva M.M., Jr., Silva M.A. Jr.,
A da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
A de Souza A.D., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
The genome sequence of the plant pathogen Xylella fastidiosa.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A MEDIINE-902058417; PubMed=2108316;
A MEDIINE-902058417; PubMed=2108316;
A Baldwin A.S., LeClair K.P., Singh H., Sharp P.A.;
Baldwin A.S., LeClair K.P., Singh H., Sharp b.A.;
T a large protein containing zinc finger domains binds to related
T sequence elements in the enhancers of the class I major
T histocompatibility complex and kappa immunoglobulin genes.";
Mol. Cell. Biol. 10:1406-1414(1990).
R PRSP; P15822; 1BBO.
InterPro; IPR00082; ZICC2H2.
R PFfam; PF00096; Zf-C2H2, 3
SMART; SW00355; Zf-C2H2, 3
R PROSITE; PS00281; ZINC_FINGER_C2H2_1; 2.
R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
W DNA-binding; Metal-binding; Zinc-finger.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequenc
01-MAR-2002 (TrEMBLrel. 20, Last annotat
DNA-binding protein (Mbp-1) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                Nature 406:151-159(2000).

EMBL; AE003967; AAF84162.1; -
HSSP; P09097; 1AB4.

InterPro; IPR002205; DNA_topoisoIV.

Probom; PD000742; DNA_topoisoIV; 1.
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TIGRFAMS; TIGR01062; parC_Gneg; 1.
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MEDLINE=94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
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"Molecular cloning of a gene, DHS1, which complements a drug-
"Molecular cloning of a gene, DHS1, which complements a drug-
hypersensitive mutation of the yeast Saccharomyces cerevisiae.";

Biosci. Biotechnol. Biochem. 58:391-395(1994).

EMBL; Z74920; CAA92201.1;

EMBL; X87331; CAA60762.1;

SGD, S000539; YOR013W.

SGD, S000539; YOR013W.
                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encodes a factor involved in mitochondrial import of yeast
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                   De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Mol. Cell. Biol. 13:6442-6451(1993).
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Matches 6; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 72.998 Million cell updates/sec June 4, 2003, 13:04:34; Search time 6.25 Seconds Run on:

1 eevvpxgmsys 11 Perfect score: Sequence:

AUDET-909-1

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

112892 segs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

		•			SUMMARIES		
Result		* Ouerv					
No.	Score	Match	Length	DB	ID	Description	ption
Н	38	73.1	1058	П	CARB FUSNN	Q8rg86	fusobacteri
7	37	ä	877	Н	SULH SCHPO	074377	schizosacch
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4	36	69.2	1498	Н	Y1A9_CLOAB	204351	clostridium
Ŋ	35	7.	2717	Н	ZEP1 HUMAN	P15822	homo sapien
y	34	65.4	788	Н	CY14_NEUCR	\sim 1	neurospora
7	34	5	_	Н	A10C HUMAN	060312	homo sapien
80	33			Н	RL20 MYCPU	098qv0	mycoplasma
თ	33	•		Н	Y990 CAMJE	P45489	
10	33			Н	AROA_VIBCH	Q9krb0	•
11	33			Н	CC37_SCHPO	094740	
12	33			Н		Q9nzm5	homo sapien
13	33				BCN5 CLOPE	P08696	clostridium
14	33			Ч	LTBS_HUMAN	P22064	
15	33			Н	RPOC_VIBCH	Q9kv29	
16	33			٦	LTBL_HUMAN	014766	_
17	33			Ч	LTB1_RAT	000018	
	32			Н	CGD2_RAT	004827	rattn
	32	•			CGD2_HUMAN	P30279	
	32			•		P30280	พนธ ส
	32				CGD1_BRARE	090459	
	32	ä			CGD1_XENLA	P50755	xenopus
	32	7			CGD2_CHICK	P49706	
	32	1			CGD2_XENLA	P53782	xenopus
	32	ŗ,			CGD1_CHICK	P55169	gallu
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	32	ä		•	CGD1_MOUSE	P25322	พาธ พ
	32	۲.			CGD1_RAT	994	
	32	ä			TOLB_HAEIN	57	haemophilus
31	32	61.5	529	Н	ENP3_HUMAN	075355	homo
	32	Η.			OAT6_HUMAN	Q9y616	_
	32	÷.		-	PRTP_HSV6U	P52384	human herpe

P32784 saccharomyc	Q62671 rattus norv	P28931 tomato aspe	P16916 escherichia	P16918 escherichia	P16917 escherichia	095071 homo sapien	P17280 chimpanzee	Q10676 mycobacteri	O59619 pyrococcus	Q9hnu2 halobacteri	005756 mycobacteri	
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34 32	35 32	•		38 32							45 31	

ALIGNMENTS

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                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
                                                                                                                                                                                                                                                                        Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                PRT; 1058 AA.
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InterPro; IPR005483; CPase_L.
InterPro; IPR005481; CPase_L. D2.
InterPro; IPR005481; CPase_L. D2.
InterPro; IPR005481; CPase_L. D3.
InterPro; IPR005481; CPase_L. N.
InterPro; IPR004362; MGS_like.
Pfam; PP00289; CPSase_L. Chain; 2.
Pfam; PP02187; CPSase_L. D3; 1.
Pfam; PP02187; CPSase_L. D3; 1.
Pfam; PP02187; CPSase_L. D3; 1.
PRINTS; PR00189; MGS; IL.
PRINTS; PR00189; CPSASE.
                                STANDARD;
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                                CARB FUSIN
                                                             QBRGB6;
CARB FUSNN
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Mood V., Gwilliam R., Relaidspace M.A., Lyne M., Lyne R., Stewart A., Rocks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., A Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., A Golins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A Hanby T., Howarth S., Huche B.J., Hunt S., Jagels K., Junes K., Jones L., Jones M., Leather S., McDeald S., McLean J., Anoney P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C., An Divor K., O'Neil S., Pearson D., Guell M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares R., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Meltjens I., Vanetreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Euchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Bertjens I., Vanetreels E., Rieger M., Schaefer M., Meller H., Wanbutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., A Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gelschuf S., Krmstrong J., Forsburg S.L., Andreworski G.V., Ussery D., Barrell B.G., Nurse P., The Genome sequence of Schizosaccharomyces pombe.";
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                                                                                                                           OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
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WANGANESE 1 AND 2 (BY SIMILARITY).
WANGANESE 2 (BY SIMILARITY).
WANGANESE 3 (BY SIMILARITY).
WANGANESE 3 (BY SIMILARITY).
                         Arginine biosynthesis; ryrrmanna ATP-binding; Manganese; Complete protecme.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
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-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 1058;
Pred. No. 6.2;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; ED7037AF77C1E39F CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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ATP (POTENTIAL)
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Probable sulfate permease C3H7.02.
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PROSITE; PS00867; CPSASE 2; 2
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074377;
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SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56995A8493371E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tobacco yellow dwarf virus (strain Australia) (TYDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL_1993 (Rel. 26, Created)
01-JUL_1993 (Rel. 26, Last sequence update)
01-CTL-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
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             -!- SIMILARITY: BELONGS TO THE SLC26A F-!- SIMILARITY: CONTAINS 1 STAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
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                                                                                                                                                                                      EMBL; AL031261; CAA20298.1; -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
                                                                                                                                                                                                                                    Pfam; PF00916; Sulfate_transp; 1.
Pfam; PF01740; STAS; 1.
PGTRFAMs; TIGRO0815; sulP; 1.
PROSITE; PS01130; SLC26A; 1.
PROSITE; PS50801; STAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96373 MW;
                                                                                                                                                                                                                                                                                                                     Iransport; Transmembrane.
IRANSMEM 133 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 VVPQGMSYA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           594 . . 877 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                  1161
2221
2221
2221
2292
3329
4424
4614
518
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i-SIMILARITY: BELONGS TO THE FISK/SPOILIE FAMILY.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATC. 824 / DSM 792 / VXM B-1787;
MREDIANG=ATC. 824 / DSM 792 / VXM B-1787;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetcbutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a
"Saquence and molecular characterization of a DNA region encoding a
mall heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                     ;
                                                                                                                                                             69.2%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.4; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168968 MW; FF42037A335A9649 CRC64;
                                                                 InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 Aa; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE007866; AAK81629.1; -. EMBL; X65276; CAA46379.1; ALT FRAME.
INTECPPO; IPRO02543; FISK SPOITIE.
Pfam; PF01880; FLSK SpOIIIE; 2.
Hypothetical protein; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-108 FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; Pubmed=8501044;
 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein CAC3709.
                                  EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 69.2%;
Similarity 60.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium acetobutylicum
                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    682
                                                                                                                                                                                                                                        2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                          7 QVVPSGINYS 16
                                                     PIR; A42452; A42452.
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                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium
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CLOAB
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0; Gaps

2; Indels

Pred. No. 23; 2; Mismatches

Score 36; Pred. No.

DB 1; Length 1498;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Biochemistry 31:3907-3917(1992).

Fiochemistry 31:3907-3917(1992).

Fiochemistry 31:3907-3917(1992).

Formal and a specific cally binds to the DNA SEQUENCE of GGACTTTCC-3. WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMBEROUS VIRAL PROMOTERS SUCH AS THOSE OF SY40, CWY, OR HIV1.

IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MGC. INTERLEUKIN-2 RECEPTOR, AND INTERPERON-BETA GENES. IT MAY ACT IN T-CELL ACTIVATION.

NUCLEAR ACTIVATION: Nuclear.
                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2010 (Rel. 40, Last annotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-EP) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fan C.M., Maniatis T.; AA DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 2087-2142.
MEDLINE=92232684; PubMed=15678844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
-!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 2113-2142.
MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
                                                                                                                                           2717 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC-FINGER IN-BETWEEN.
-:- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X51435; CAA35798.1; -.
                                    1276 ÉQKIPMGMSY 1285
                                                                                                                                           STANDARD;
1 EEVVPXGMSY 10
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PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T00497; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                 HIVEPI OR ZNF40.
                                                                                                                                                                                                                                                                                                              PRDII-BF1)
                                                                                                                                           HUMAN
                                                                                                                                                            P15822;
                                                                                                                     ZEP1_HUMAN
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30-MAY-2000 (Rel. 39, Created)
15-UTN-2002 (Rel. 41, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Potential phospholipid-transporting ArPase VC
(Aminophospholipid translocase VC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                 Glycoprotein.
                                                                                                                                                                                                                                                                                       POTENTIAL
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                                                                                                                                                                                      InterPro; IPR001902; Sulfate_transp. Pfam; PF00916; Sulfate_transp; 1. TIGRPAMs; TIGR00815; SulF; 1. Pransport; Transmembrane; Glycoprote:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21225279; PubMed=11326269;
                                                                                                                                                     EMBL; M59167; AAA33615.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 337-1499 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGMSYS 11
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                                                                                                                                                                       PIR; A37956; A37956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   788 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oshimura M.;
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MEDLINE=94188926; PubMed=8140616;

A Sandal N.N., Marcker K.A.;

Sandal N.N., Marcker K.A.;

Sandal N.N., Marcker K.A.;

T "Similarities between a soybean nodulin, Neurospora crassa sulphate

T "rends Blochem. SG1. 19:19-19(1994).

L Trends Blochem. SG1. 19:19-19(1994).

-!- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.

-!- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.

-!- FUNCTION: Highly expressed, but only in cells subject to sulfur cell initiation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.

-!- MISCELLANGOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.

-!- SIMILARITY: BELONGS TO THE SIC26A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-91129256; PubMed-1825178;
MEDLINE-91129256; PubMed-1825178;
MEDLINE-91129256; PubMed-1825178;
MEDLINE-91129256; PubMed-1825178;
Melter J.S., Jarani G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in
                                                                                                    SMAKT; SHOUSS); ALL CALL 1, 4.

PROSITE; PSOOLSS; ZINC_FINGER_C2H2_2; 4.

PROSITE; PSSO157; ZINC_FINGER_C2H2_2; 4.

Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;

Nuclear protein; Repeat; 3D-structure.

DOMAIN 406 428 CZH2-TYPE.

ZINC FINGERS.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 1; Length 2717; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                            C2H2-TYPE.
POLY-SER.
C2HC-TYPE (POTENTIAL).
ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Sulfate permease II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             788 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 30:1780-1787(1991)
                                 InterPro, IPR000822, Znf C2H2.
Pfam, PF00096; zf-C2H2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%;
                                                                          PRINTS; PR00048; ZINCFINGER.
                                                                                                C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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 Genew; HGNC:4920; HIVEP1
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2109
2139
2088
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2109.
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                                                                                              SMART; SM00355; ZnF
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Best Local Similarity
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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SEQUENCE FROM N.A.

MEDLINE=21313119; PubMed=11353404;

Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;

Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;

"The human aminophospholipid-transporting ATPase gene ATP10C maps

"The human aminophospholipid-transporting ATPase gene ATP10C maps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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MEDLINE=98290545; PubMed=9628581;
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 788;
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"prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5.31-39(1998).
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- TISSUE SPECIFICITY: Wide expression, with highest levels in kidney, followed by lung, brain, prostate, testis, ovary, and small intestine.
-!- DISBASE: Defects in ATP10C may be a cause of Angelman syndrome (AS), also known as 'happy puppet syndrome'.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR001454; Hlgnase/hydrlase.
InterPro; IPR00125; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
PROSITE; PS001154; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
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AAK33100.1;
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Multigene family.
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                                                                                                                                                    ö
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma pulmonis.";
Mycleic Acida Res. 29:2145-2153(2001).
Nucleic Acida Res. 29:2145-2153(2001).

-i- FUNCTION: THIS PROFEND BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL
SUBDART: TT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS
OF THAT SUBUNIT (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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0
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 PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                  65.4%; Score 34; DB 1; Length 1499; 72.7%; Pred. No. 62;
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Mypulist; MYPU 2610;
InterPro; 1 WPO1081; Ribosomal L20.
Pfam; PF00453; Ribosomal L20; I.
PRINTS; PR00062; RIBOSOMALL20.
ProDom; PD002389; Ribosomal L20; 1.
TIGREAMS; TIGREAMS; TIGNE 120; 1.
PROSITE; PS00937; RIBOSOMAL L20; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
427 427 PHOSPHORYLATION (BY SIMILARI)
1031 1031 MAGNESIUM (BY SIMILARITY).
1035 MAGNESIUM (BY SIMILARITY).
470 POLY-GLU.
248 388 Q -> R (IN REF. 3).
1499 AA, 167687 MW, D4996A4D0635A6BD CRC64;
                                                                                                                                                    3; Indels
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15-UNN-2002 (Rel. 41, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L20.
RPLT OR MYPU_2610.
                                                                                                                                                     0; Mismatches
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nes 7; Conservative
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                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
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RL20 MYCPU
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RESULT

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CC37 SCHPO
094740;
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                                                                                                                                                                                MEDLINE=20150912; PubMed=10688204; Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G., "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                           Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase)
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NCBI_TaxID=666;
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benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
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SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
         Y990_CAMJE STANDARD; PRT; 253 AA. P45489; Q9PNVO; 01-NOV-1995 (Rel. 32, Created) CCT-2001 (Rel. 40, Last sequence update) 116-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein Cj0990c.
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STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; Pubmed=10952301;
                                                                                                                                                                                                                                                                         reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                                                                                                                                                                                  MEDLINE=95247673; PubMed=7730270;
Hani E.K., Chan V.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL139076; CAB73246.1; -. EMBL; Z36940; CAA85392.1; -.
                                                                                                                                                                                                                                                                                                         SEQUENCE OF 160-253 FROM N.A. STRAIN=ATCC 43431 / TGH 9011;
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                                                                                                 Campylobacter jejuni
                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=NCTC 11168;
                                                                                                                                  NCBI_TaxID=197;
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Y990 CAMJE
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D. Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Pragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972;
MEDLINE=21848401; PubMed=11859360;
Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgoot V., Gwilliam R., Hayles J., Baker S., Basham D., Browns J., Bawm S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPAC986.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00275; EPSP syntase; 1.
ProDom; PD001867; EPSP syntase; 1.
ProSITE; PS00104; EPSP SYNTHASE 1; 1.
PROSITE; PS008865; EPSP SYNTHASE 2; 1.
Aromatic amino acid biosynthesis; Transferase; Complete proteome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Westwood P.K., Preston N.C., Fantes P.A.; "Schizosaccharomyces pombe cdc37 gene."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sixth step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001986; EPSP syntase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004251; AAF94882.1; -.
TIGR; VC1732; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                  Nature 406:477-483 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
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MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.V., Ucki K., Billings R. Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                                                                    -i- SUBUNIT: Porms a complex with Hsp90. Interacts with a number of kinases (By similarity).
-i- SUBCELLULAR LOCATON: CYCOPISSMIC (By similarity).
-i- SIMILARITY: BELONGS TO THE CDC37 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Q9NZM5; QNPP1; Q9NFR4; Q9UFI2; Q9BTC6; Q9HAX6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 1; Length 466; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ132376; CAB38757.1; -.
EMBL, AL049769; CAB42371.2; -.
Chaperone; Cell division. Cell cycle.
SEQUENCE 466 AA; 52554 WW; 647238B34CABB3C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ132377; CAB38758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSR2 HUMAN
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                                                                                                                                                                                                                                                                                                R -> Q.

/FTIG=VAR 011486.

GSS -> HEG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEQLWEKLAKQGELPREVRRAQARLINPSATRAKPGPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IN REF. 3).

A > S (IN REF. 2; AAH04229).

D -> H (IN REF. 3).

PEGNILRDRFKSFQRRNMIEPRERAKFKRYKVKLVEKRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REIQ -> VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP
WAGPVGPMPRG (IN REF. 5).
EGNILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVERP -> SGRSSYGRSWPSRASSPGGAQGPSPVAQPFCN
                                                                                                 SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGPNPAPGHRIAA (IN REF. 3).
SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWPGCLFPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7F18923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 63.5%; Score 33; DB Similarity 60.0%; Pred. No. 30; 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF182076; AAF62873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC004229; AAH04229.1; -. BC006311; AAH06311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC010095; AAH10095.1; -. EMBL; AF296124; AAG30413.1; -.
                                                                                                                                                                                              Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 AA; 54417 MW;
                                                                                                                                                                                                                                                                          SEQUENCE OF 218-477 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF296124; AAG30413.1;
EMBL; AL359335; CAB94786.1;
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Genew; HGNC:4333; GLTSCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL122063; CAB59242.1
region.";
Genomics 64:44-50(2000).
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191
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                                    SEQUENCE FROM N.A.
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417
433
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                                                   TISSUE=Muscle:
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                                                                                                                                                                                   infection.
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P22064;
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DOMAIN
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Garnier T., Cole S.T.;
"Studies of UV-inducible promoters from Clostridium perfringens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE=87057020; PubMed=2877971;
Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium berfringens and molecular genetic analysis of the bacteriorin-annohim mone "."
                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes, Clostridia; Clostridiales, Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96699 MW; F4E5E8971C31C6C6 CRC64;
                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                     890 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacteriocin-encoding gene.";
J. Bacteriol. 168:1189-1196(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88336297; PubMed=2901768; Garnier T., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00287; SH3b; 3. Antibiotic; Bacteriocin; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2:607-614 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003646; SH3_bac.
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EMBL; M32882; AAA98249.1; -.
PIR; A30481; A30481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                        Clostridium perfringens.
                                                                                                                                       STANDARD;
                                  239 EVAPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          869
2 EVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                            01-JAN-1988 (Rel. 01-OCT-1994 (Rel. Bacteriocin BCN5.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol.
                                                                                                                                                                                                                                                                                               Plasmid pIP404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CPN50;
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P08696;
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MEDLINE=90275601; PubMed-2150783;

MEDLINE=90275601; PubMed-2150783;

Mayazono K., Claesson-Welsh L., Heldin C.-H.;

Myazono K., Claesson-Welsh L., Heldin C.-H.;

TGF-beta 1 binding protein: a component of the large latent complex of TGF-beta 1 with multiple repeat sequences.";

Cell 61:1051-1061(1990)

C. I- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS COMPOSED OF THE TGF-BETA1 MOLECULE NOWOVALENTY ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-BETA1-BP. TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.

C.I- ALTERNATIVE PRODUCTS: 2 isoforms; a short form (shown here) and a long form (AC 014766); are paroduced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00151; Asx_hydroxyl.

R InterPro; IPR00151; EGF_like.

DR InterPro; IPR001511; EGF_Ca.

DR InterPro; IPR0012812; Fibril-assoc.

R InterPro; IPR0012812; Fibril-assoc.

DR Ffam; PP00683; TB; 4.

DR SMART; SM00179; EGF_Like; 4.

DR SWART; SM00179; EGF_Like; 4.

DR SWART; SM00109; EGF_Like; 4.

DR PROSITE; PS00100; ASX_HYDROXYL; 13.

R PROSITE; PS01187; EGF_Li.

DR PROSITE; PS01186; EGF_Z; 11.

DR PROSITE; PS01186; EGF_Z; 11.

DR PROSITE; PS01187; EGF_CA; 15.

W Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal;

T SIGNAL

SIGNAL

T SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
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                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UWN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1S precursor
(Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LATENT TRANSFORMING GROWTH FACTOR BETA
                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EGF-LIKE 2, C
EGF-LIKE 3, C
EGF-LIKE 4, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M34057; AAA61160.1; -. PIR; A35626; A35626.
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GlycoSuiteDB; P22064; -.
Genew; HGNC:6714; LTBPI.
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LTBS HUMAN
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REPEAT C.

REFEAT C.

EGF-LIKE 15.

EGF-LIKE 15.

CELL ATACKHENT SITE (POTENTIAL).

BY SIMILARITY.

BY SIMILAR
                                                                                                 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL)
                                                EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL)
            (POTENTIAL)
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N-LINKED (GLCNAC. . . )
N-LINKED (GLCNAC. . . . )
N-LINKED (GLCNAC. . . )
N-LINKED (GLCNAC. . . )
 EGF-LIKE 6,
EGF-LIKE 7,
EGF-LIKE 8,
EGF-LIKE 9,
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STRAIN=E1 Tor Nic961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelboerg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: DNA-DEPENDENT RNA POLYWERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (By similarity).
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                              Gaps
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-i. SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN (By similarity).
-i. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
VCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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Pred. No. 93;
3; Mismatches 2; Indels
           Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01853; RNA_pol_A; 1.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
                                                Indels
                DB 1;
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              Score 33;
Pred. No. 9
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HSSP, Q9KWUG, 1HQM.
TIGR; VC0329; -
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50.0%;
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Query Match
Best Local Similarity 45...
5; Conservative
                                                                                                                                                                                                             STANDARD;
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                                                                                                                        399 KEICPGGMGYT 409
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SEQUENCE 1401 AA
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Q9KVZ9;
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RPOC_VIBCH
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Search completed: June 4, 2003, 13:11:44 Job time: 7.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:08:49; Search time 11 Seconds (without alignments) 96.134 Million cell updates/sec

1 eevvpxgmsys 11 AUDET-909-1 52 Title: Perfect score: Sequence: Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΩI	Description
-	38	73.1	3472	7	T31308	
7	37	71.2	840	7	T39116	probable sulfate p
ю	37	71.2	877	~	T40413	sulfate permease -
4	36		102	7	A42452	V1 protein - tobac
ഗ	36	69.2	1498	~	B97355	DNA segregation AT
9	35	67.3	225	7	S57810	hypothetical prote
7	35	67.3		7	T24111	hypothetical prote
80	35			7	S22293	zinc finger protei
6	35	67.3		N	H82691	topoisomerase IV s
10	35	67.3	2717	7	A34203	DNA-binding protei
11	34	65.4		N	854619	hypothetical prote
12	34	ທ		N	H69491	g
13	34	65.4	544	N	C82900	probable ABC subst
14	33	63.5	94	N	140758	hypothetical prote
15	33	ë.	116	N	E90544	_
16	33	3	165	N	D69493	
17	33	Э.	253	~	C81374	
18	33	ω.	259	0	T34536	
19	33	ω.	284	7	S75817	hypothetical prote
20	33		298	7	T47670	_
21	33	Э.	368	~	F72281	hypothetical prote
22	33	ω.	426	7	D82163	之
23	33	ω.	466	7	T43653	cdc37 protein - fi
24	33		653	7	D82352	iron(III) ABC tran
25	33	ω.	890	~	A30481	bacteriocin BCN5 -
26	33	33	1028	~	AF3286	ATP-dependent DNA
27	33	63.5	1152	7	70	conserved hypothet
28	33		1394	7	562	transforming growt
29	33	63.5	1401	N	G82336	

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0; Gaps

Query Match 71.2%; Score 37; DB 2; Length 840; Best Local Similarity 77.8%; Pred. No. 21; Matches 7; Conservative 1; Mismatches 1; Indels

||| ||||: 135 VVPQGMSYA 143 3 VVPXGMSYS 11

Db ò

hypothetical prote	masking protein pr	hypothetical prote	transport protein	rho protein GDP-di	hypothetical prote	cyclin D2 - rat	cyclin D2 - rat	cyclin D2 - mouse	cyclin D2 - human	cyclin D1 - Africa	cyclin D2 - Africa	cyclin D2 - chicke	cyclin D1 - zebra	cyclin D3 - human	cyclin D1 - human
T04456	A38261	E97333	PQ0616	T01457	B72481	JC4011	158372	A41984	A42822	S57922	S57925	JC4579	862730	B42822	A38977
~	~	N	~	0	N	~	7	7	~	0	N	~	0	~	N
1548	1712	84	175	223	279	288	288	289	289	291	291	291	291	292	295
63.5	63.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5
33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	T31308
	hypothetical 367K protein - Cenarchaeum symbiosum
	C;Species: Cenarchaeum symbiosum
	C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_cnange 18-Feb-2000
	C;Accession: T31308
	R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, K.V.
	J. Bacteriol. 180, 5003-5009, 1998
	A,Title: Genomic analysis reveals chromosomal variation in natural populations of the unc
	A; Reference number: Z20994; MULD: 984Z2450; PMLD: 9/48430
	A;ACCESSION: 1131308
	A)Status; premiminary; cramstated from 55 minu, one
_	A; Molecule Cype: DNA
	A; Kesidues: I-34/Z SSCH>
	A;Cross-reterances: MALL-AFRUSJULX, NLD:G359555; FLD:G3039539; FLDN:ANCOZ039.1 C.Sunerfamily: Cenarchaeum symbiosum hybothetical 367K Drotein
	Similarity 54.5%;
	of Collect Vactors 1, inclinations 1, inclination 10
	Qy 1 EEVVPXGMSYS 11
	Db 2294 EVVIPRGITES 2304
	RESULT 2
	T39116
	probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
	C;Species: Schizoseaccharomyvdes pombe C:Date: 03-Dec-1999 #semience revision 03-Dec-1999 #text change 03-Dec-1999
	C.Accession: T39116
	R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
	submitted to the EMBL Data Library, November 1999
	A.Reference number: Z21829
	A-Arcessicur: 159116 A-Status: oreliminary: translated from GB/EMBL/DDBJ
	A Molecule type: DNA
	A; Residues: 1-840 < HUN>
	A;Cross-references: EMBL:AL13279; PIDN:CABG0015.1; GSPDB:GN00066; SPDB:SPAC869.05c
	Ajexperimental source: strain 9/2n-; cosmig csoy C.Generics:
	A. Gene: SPDB:SPAC869.05c
	A,Map position: 1

Gaps

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A; Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Lycopersicon esculentum (tomato)
Cibate: 28-0c1-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
Cibate: 28-0c1-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
Rimiligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Accession: S5780
A;Status: preliminary, nucleic acid sequence not shown
A;Accession: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
R;Percy, C.
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C;Species: Rattus norvegicus (Norway rat)
C;Decies: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22293; 178666
C;Accession: S22293; 178666
R;Mitchelmore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-225 <MIL>
A;Cross-references: EMBL:U20592; NID:g924625; PIDN:AAA80497.1; PID:g924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
            Length 1498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%; Score 35; DB 2; Length 225; 54.5%; Pred. No. 13; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h similarity 50.0%; Pred. No. 26; 5; Conservative 3; Mismatches 2: Indela
                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein precursor (clone TPP11) - tomato
    DB 2;
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                                    63;
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                                                                                2; Mismatches
        Score 36;
Pred. No. 6
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    69.2%;
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Best Local Similarity 54.5.
Best Local 6. Conservative
                                                                                6; Conservative
                                                                                                                                                                                                                                    1276 EQKIPMGMSY 1285
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32 DEVVPNGKTYA 42
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                                                                                                                                                            1 EEVVPXGMSY 10
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A;Accession: T24111
Query Match
Best Local Similarity
Matches 6; Conserva
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Matches 5; Conserv
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A; Residues: 1-425 <WIL>
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A;Gene: CESP:R10D12.10
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DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported] - Clos Cyspecies (lostridium acetobutylicum (j.Species (lostridium acetobutylicum (j.Species 10.5))

Cyspecies 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

Cyscession: B97355

Fivoliliapy J.; Bareton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V1 protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T40413
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-877 <LYN>
A;Residues: 1-877 <LYN>
A;Residues: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
C;Genetics:
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A;Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics: A;Genetics: A
                                                                                                                                    C;Species: Schizosaccharomyces publicosaccharomyces pumbe;
C;Species: Schizosaccharomyces pumbe
C;Accession: T40413
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
A;Reference number: Z21926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Molecule type: DNA
A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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                                                                T40413 sulfate permease - fission yeast (Schizosaccharomyces pombe)
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Matches 7; Conservative
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A42452 Vl prot

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A; Experimental source: strain S288C
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Matches 6; Conservative
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2405 VVPAGLTYS 2413
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Nature 406; 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Recession: H82691
A;Scatus: preliminary
A;Recidues: 1.749 <SIM>A;Scatus: preliminary
A;Residues: 1.749 <SIM>A;Residues: 1.749 <SIM>A;Residues: 1.749 <SIM>A;Residues: Type: DNA
A;Residues: 1.749 <SIM>A;Residues: Carraro, DNA;Residues: GB:AE003967; GB:AE003849; NID:99106347; PIDN:AAF84162.1; GSPDB:GNO1
A;Residues: J.749 <SIM>A;Residues: GB:AE003967; GB:AE003849; NID:99106347; PIDN:AAF84162.1; GSPDB:GNO1
A;Residues: L.749 <SIM
A;Residues: L.749 <SIM
A;Residues: L.749 <SIM
A;Residues: GB:AE003967; GB:AE003849; NID:99106347; PIDN:AAF84162.1; GSPDB:GNO1
A;Residues: L.749 <SIM
A;Residues: L.749 <SIM
A;Residues: L.740 <SIM
A;Residu
A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: 158280; MUID:91187610; PMID:1901405
A;Accession: S22293
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: XF1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        topoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: Xylella fastidiosa
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                               A;Cross-references: EMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520 A;Note: the authors did not translate the codon for residue 1 C;Superfamily: HIV-EP2 enhancer-binding protein C;Superfamily: HIV-EP2 enhancer-binding protein C;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 2; Length 670; Pred. No. 43; 2; Mismatches 1; Indels
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Pred. No. 48;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.3%;
Best Local Similarity 66.7%;
Matches 6; Conservative ;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMSYS 11
                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-670 <MIT>
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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A,Residues: 1-156 <DEW>
A,Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01:
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N;Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C;Accession: H69491
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A; Residues: 1-156 < DEH>
A; Residues: 1-156 < DEH>
A; Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R; de Haan, M.; Grivell, L.A.; Maarse, A.C.
B; de Haan, M.; Grivell, B; de B;
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Cispecies: Saccharomyces cerevisiae
Cibacte: 08-401-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
Citacession: S54619; S66879
Ride Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Reference number: S54619
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C,Superfamily: hypothetical protein YOR013w
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RESULT 15 E90544

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Nature 390, 364-370, 1997
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A,Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A,Reference number: A69250; MUD:98049343; PMID:9389475
A,Accession: H69491
A,Accession: H69491
A,Accession: H69491
A,Kesidue: preliminary; nucleic acid sequence not shown; translation not shown A,Residues: 1-252 <KLE>
A,Residues: 1-252 <KLE>
A,Cross-references: GB,AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264866 C;Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: C82900 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. Bubmitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-544 <GLA>
A;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
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A; Reference number: I40758; MUID: 95247673; PMID: 7730270
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C'Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C'Accession: 140758; 547317
E.K., Chan, V.L.
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
A;Residues: 1-94 <RES>
A;Cross-references: EMBL:Z36940; NID:g533805; PIDN:CAA85392.1; PID:g535806
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Pred. No. 13;
2; Mismatches 2; Indels
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Best Local Similarity 75.v.
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 EVIPAGMS 88
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A;Genetic code: SGC3
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C,Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: B90544 C;Accession: B90544 C;Accession: B90544 N:Chambaud, I:; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #text_change 03-Aug-2001
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A,Genetic code: SGC3
C,Superfamily: Escherichia coli ribosomal protein L20
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les 7; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-116 < KUR>
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                   June 4, 2003, 13:11:19; Search time 183 Seconds (without alignments) 38.754 Million cell updates/sec
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1: \cgn2 6/ptodata/1/paa/PCTUS COMB.pep:*
2: \cgn2 6/ptodata/1/paa/USOG =COMB.pep:*
3: \cgn2 6/ptodata/1/paa/USOG =COMB.pep:*
4: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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	Description	Sequence 33980, A	Sequence 36185, A	Sequence 38532, A	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli
SUMMARIES	D	PCT-US01-08631-33980	PCT-US01-08631-36185	PCT-US01-08631-38532	US-09-408-020-4	US-10-027-801-4	US-10-027-806-4
	DB	-	٦	Н	18	24	24
	% Query Match Length DB	1022	1022	1022	3472	3472	3472
d	Query Match	76.9	76.9	76.9	73.1	73.1	73.1
	Score	40	40	40	38	38	38
	Result No.	н	~	m	4	2	9

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### ALIGNMENT

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RESULT 1
PCT-USO1-08631-33980

Sequence 33980, Application PC/TUSO108631

GENERAL INPORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYBEPTIDES
FILE REPERENCE: 212-72-049

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PLING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEATURE:
CORGANISM: Homo sapiens
FRATURE:
NAME/KEY: DOMAIN

LOCATION: (986). (1003)

OTHER INFORMATION: Ednc finger C2H2 type, domain identified by OTHER INFORMATION: 16.07

NAME/KEY: DOMAIN

NAME/KEY: DOMAIN

COTHER INFORMATION: Zinc finger, C2H2 type domain identified by PFam, accession

COTHER INFORMATION: 210c finger, C2H2 type domain identified by PFam, accession

COTHER INFORMATION: Zinc finger, C2H2, E-value=4.2e-28, PFam score of 106.8
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; Sequence 4, Application US/09408020
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/10027801
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.01
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2294 EDVIPRGISFS 2304
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Matches 6; Conservative
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                                             ORGANISM: Homo sapiens
                                                                                       NAME/KEY: DOMAIN
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    LENGTH: 1022
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US-09-408-020-4
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US-10-027-801-4
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OTHER INFORMATION: Zinc finger C2H2 type, domain proteins. domain identified by
OTHER INFORMATION: eMATRIX, accession number BL00028, p-value=8.714e-09, raw score
OTHER INFORMATION: 16.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: DOMAIN
LOCATION: (472)..(1007)
OTHER INFORMATION: Zinc finger, C2H2 type domain identified by PFam, accession
OTHER INFORMATION: name zf-C2H2, E-value=4.2e-28, PFam score of 106.8
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                                                                                                    76.9%; Score 40; DB 1; Length 1022; 80.0%; Pred. No. 1e+02; tive 1; Mismatches 1; Indels
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80.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyeeq, Inc.
ITTLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILLS REFERENCE: 2127-2-049
FILLS REFERENCE: 2127-2-049
CURRENT APPLICATION NUMBER: PCT/USO1/08631
CURRENT FILING DATE: 2001-03-30
PRIOR PELLING DATE: 2000-03-31
PRIOR PELLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLSLOM
SEQ ID NO 36185
LENGTH: 1022
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILE REPERENCE: 2127-049
CURRENT APPLICATION NUMBER: 90/540,217
FURDR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 38532
                                                                                                                                                1; Indels
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                   ; LOCATION: (1). T. (1022)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-33980
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OTHER INFORMATION: Xaa = X or * as defined in Table 2
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                                                                              Query Match
Best Local Similarity 80.0%;
Conservative
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Matches 8; Conservative
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NAME/KEY: misc_feature
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LOCATION: (986)..(1003)
OTHER INFORMATION: Zinc finger C2H2 type, domain proteins. domain identified by
OTHER INFORMATION: MATRIX, accession number BL00028, p-value=8.714e-09, raw score of
OTHER INFORMATION: 16.07
NAME/KEY: DOMAIN
                                                                                                                                                              LOCATION: (472)...(1007)
OTHER INFORMATION: Zinc finger, C2H2 type domain identified by PFam, accession OTHER INFORMATION: name zf-C2H2, E-value=4.2e-28, PFam score of 106.8
NAME/KEY: (110-110)...
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APPLICANT: Feldman, Robert A.
TITLE OF INVENTION: WIGHER: US(9/408,020
CURRENT FILING DATE: 1999-09-29
EARLIER APPLICATION NUMBER: 60/102,294
EARLIER APPLICATION NUMBER: 60/102,294
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Swanson, Robert A.
APPLICANT: Schleger, Christa
APPLICANT: Schleger, Christa
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT FILING DATE: 2001-12-21
PRIOR PPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%; Score 40; DB 1; Length 1022; 80.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa = X or * as defined in Table 2 PCT-US01-08631-38532
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LENGTH: 3472
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                  RESULT 8
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Sequence 4, Application US/10029120;
GENERAL INFORMATION:
APPLICANT: Swanson, Rohart A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/029,120
CURRENT FILING DATE: 2001-12-21
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 3472
                                                                                                                                                                                                                                                                                                      Sequence 4. Application US/10027806;
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.;
APPLICANT: Feldman, Robert A.;
APPLICANT: Feldman, RObert A.;
APPLICANT: Schleper, Christa
TITLE OF INVENTON: UNCLETC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER PPLICATION NUMBER: 09/408,020
PRIOR APPLICATION WIMPER: FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 3472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%; Score 38; DB 24; Length 3472; 54.5%; Pred. No. 1.1e+03; Live 4; Mismatches 1; Indels (
                                                                                           Score 38; DB 24; Length 3472;
Pred. No. 1.1e+03;
4; Mismatches 1; Indels C
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ORGANISM: Cenarchaeum symbiosum
                      TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                 73.1%;
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Best Local Similarity 54.57
Conservative
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                                                                              Query Match
Best Local Similarity 54.5.
Best Local 6; Conservative
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
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                                                                                                                                                                             1 EEVVPXGMSYS 11
LENGTH: 3472
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US-10-029-120-4
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                                                         US-10-027-801-4
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APPLICANT. BONDAZI, VIVIEN
APPLICANT. BONDAZI, VIVIEN
APPLICANT. BONDAZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000450,
CURRENT APPLICATION NUMBER: US/60/196,710
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7166
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6207
LENGTH: 129
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000210
CURRENT APPLICATION NUMBER: US/60/177,646
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 4226
NGSTOL 10

Sequence 4, Application US/10034623

Sequence 4, Application US/10034623

GENERAL INFORMATION:

APPLICANT: Swanson, Robert A.

APPLICANT: Schleper, Christa

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

FILE REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/034,623

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/408,020

PRIOR APPLICATION NUMBER: 09/102,294

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%; Score 38; DB 24; Length 3472; 54.5%; Pred. No. 1.1e+03; tive 4; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%; Score 36; DB 27; Length 129; 70.0%; Pred. No. 64; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 6207, Application US/60196710; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5.
Pest Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 70.v.
7, Conservative
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2294 EDVIPRGISFS 2304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: HUMAN
US-60-196-710-6207
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US-60-196-710-6207
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Gaps
                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fahy, Edin D.
APPLICANT: Fahy, Edin D.
APPLICANT: Tango, Bing
APPLICANT: Chang, Bing
APPLICANT: Tango, Bing
APPLICANT: Tango, Bradford W.
APPLICANT: Taylor, Seven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnorck, Dale E.
ITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERBRENCE: 660088.465P2
FURRENT APPLICATION NUMBER: 1202-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gooth, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Tahny, Bing
APPLICANT: Tahny, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Lardford W.
APPLICANT: Gibson, Lardford W.
APPLICANT: Gibson, Lardford W.
APPLICANT: Warnock, Dale E.
ITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERRINCE: 660088.466F93
CURRENT APPLICATION NUMBER: US/60/412,418
CURRENT APPLICATION NUMBER: US/202-09-20
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version 4.0
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                            Score 36; DB 15; Length 382;
Pred. No. 2.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.2%; Score 36; DB 27; Length 401; Best Local Similarity 70.0%; Pred. No. 2.4e+02; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                    Sequence 2598, Application US/60389987
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2598, Application US/60412418; GENERAL INFORMATION:
                               69.2%;
                         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 70.0
Pest Local 7; Conservative
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                                                                                                                                                                             332 LIPEGMSYS 340
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                                                                                                                              3 VVPXGMSYS 11
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US-60-389-987-2598
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; ORGANISM: Homo sapiens
US-60-412-418-2598
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LENGTH: 401
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OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32486, Application US/10029386
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sarron G.
APPLICANTON: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQ ID NO 32486
LENGTH: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVEXTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVEXTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-.005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO AF002994.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUE 5.00e-46
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3738, Application US/09134000A; GENERAL INFORMATION:
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LENGTH: 382
TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                               Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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97 KEVVPTGHSY 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                     TYPE: PRT
ORGANISM: HUMAN
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               SEQ ID NO 2588
LENGTH: 140
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263 KEVVPTGHSY 272

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RESULT 15
US-10-219-999-58270
; Sequence S8270, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Joshua
; APPLICANT: APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REPREENCE: 38-10(52726)C;
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; SEQ ID NO S8270
; LEMORTH: 160
; TYPE: PRT
; ORGANISM: Zea mays
US-10-219-999-58270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.3%; Score 35; DB 26; Length 160; Best Local Similarity 66.7%; Pred. No. 1.3e+02; Matches 6; Conservative 2; Mismatches 1; Indels
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Search completed: June 4, 2003, 13:27:19 Job time: 185 secs 2 EVVPXGMSY 10 |::| |||| 23 ELLPVGMSY 31 셤 ò

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Sequence 4, Application US/10034623
Publication No. US2020198365A1
GENERAL INFORMATION:
APPLICANT: Feldman, Robert A.
APPLICANT: Schlegper, Christa
TITLE OF INVENTION: UUCLEIC ACIDS AND PROTEINS FROM CENARCHABUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
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Sequence 108, App
Sequence 184, App
Sequence 108, App
Sequence 108, App
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Sequence 4, Appli
Sequence 4, Appli
Sequence 73, Appl
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Sequence 53, Appl
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Sequence 1061, Ap
Sequence 4, Appli
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Sequence 4, Appli
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                                                                                                                         (without alignments)
79.694 Million cell updates/sec
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Sequence 108,
Sequence 26,
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                                                                                                      June 4, 2003, 13:13:35 ; Search time 14.25 Seconds
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PUT.NEW FUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6.NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6.NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-027-801-4

US-10-101-464A-73

US-10-11-464A-73

US-10-11-464A-73

US-10-90-92-004-108

US-09-92-0004-108

US-10-000-489-108

US-10-000-489-108

US-10-000-489-108

US-10-000-489-108

US-10-000-986-108

US-09-947-387-66

US-09-947-387-66

US-10-024-066-2

US-10-024-066-2
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US-09-925-300-1061
US-09-923-304-4
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                                                                                                                                                                                                                                                                                                     392085 seqs, 103240269 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                   Sequence:
                                                                                                        Run on:
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WS-10-027-806-4

Sequence 4, Application US/10027806

Sequence 4, Application US/10027806

Sequence 4, Application US/202016047641

Sequence 4, Application William

APPLICANT: Swanson, Ronald V.

APPLICANT: Schleper, Christa A.

TITES OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

FILE REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/027,806

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/408,020

PRIOR APPLICATION NUMBER: BARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 3472

TYPE: PRT

CORANISM: Cenarchaeum symbiosum
US-10-027-806-4
                           Sequence 10384, A Sequence 878, Appl Sequence 878, Appl Sequence 114, Appl Sequence 5124, Appl Sequence 20, Appl Sequence 314, Appl Sequence 6349, Appl Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 10439, Appl Sequence 1130, Appl Sequence 1130, Appl Sequence 68, Appli Se
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  Sequence 2, Appli
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Sequence 85, Appl
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Pred. No. 1.2e+02;
4; Mismatches 1; Indels
0 US-09-925-731-2

0 US-09-815-244-10384

US-10-151-736-4

US-10-092-154-878

0 US-09-948-080-14

US-09-986-480-171

US-09-986-480-171

US-09-986-480-171

US-09-986-480-171

US-09-986-480-171

US-09-986-480-171

US-09-9815-242-10697

US-09-975-139-5

US-09-915-242-10439

US-09-915-242-10439

US-09-915-242-10439

US-09-915-242-10439

US-09-912-020-340

US-09-912-020-340
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US-09-853-161-85
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54.5%;
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2294 EDVIPRGISFS 2304
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    1 EEVVPXGMSYS 11
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Midgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT PILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR PLING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: FCT/USON/00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10027801
; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
; GENERAL INPORMATION:
    APPLICANT: Swanson, Rohaft A.
    TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
    TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
    PILE REFERENCE: DCORP.002A
; CURRENT APPLICATION NUMBER: US/10/027,801
; CURRENT APPLICATION NUMBER: EARLIER PELING DATE: 1999-09-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Fast5EQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
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                                                                                                                                                                                                                                                                                                                             73.1%; Score 38; DB 9; Length 3472; 54.5%; Pred. No. 1.2e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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54.5%; Pred. No. 1.2e+02;
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTEEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 73, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|:| |:|:|
2294 EDVIPRGISFS 2304
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Matches 6; Conservative
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
Matches 6; Conservative
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US-10-101-464A-73
                                                                                                                                                                                                              LENGTH: 3472
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                                                                                                                                                                                                                                                                                        US-10-034-623-4
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; Sequence 108, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUNAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91. US2.REG
CURRENT FPLING DATE: 2001-08-06
RIOR RAPPLICATION NUMBER: US 60/302,277
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR SEQING DID NOS: 112
SOFTWARE: JPatent
SOFTWARE: JPatent
TENGRAPH A79
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GENERAL INFORMATION:

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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTOR: GOAL

CURRENT APPLICATION NUMBER: US/10/214,766

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,734

PRIOR APPLICATION NUMBER: US 60/311,734

PRIOR ELING DATE: 2010-08-09

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                      Length 947;
                                                                                                                                                                                                           Query Match 65.4%; Score 34; DB 9; 1
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 60.v.
Best Local 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 EFVIPAGOSY 232
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ORGANISM: Homo sapiens
US-09-924-340-108
                                                                                                                         TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                          686 VMPSGISYS 694
                                                                                                                                                                                                                                                                                                               3 VVPXGMSYS 11
                                                                                                                                                                         US-10-101-464A-73
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US-10-214-766-43
                                                                             SEQ ID NO 73
LENGTH: 947
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US-10-00-482-108

Sequence 108, Application US/10000489

Publication No. US20030092011A1

GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane.

APPLICANT: Tanaka, Hiroaki

TILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.USG.DIV.

CURRENT APPLICATION NUMBER: US/10/000,489

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: PCT/IB01/01715

PRIOR PILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-13

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SOFTWARE: JPatent

SEQ ID NO 108

LEASTH: 478

LEASTH: 478
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <university control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%; Score 33; DB 9; Length 478; 60.0%; Pred. No. 1.4e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 9; Length 478;
Pred. No. 1.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 478 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: cUnknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-746-783-184
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Milasincic, Debra J. REGISTRATION NUMBER: 46,931 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 60.0°
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US-10-000-489-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-000-489-108
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US-09-992-600A-108

Sequence 108, Application US/09992600A

Publication No. US20030027161A1

GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Benjamin, Stephane
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hircaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
TITLE REFERENCE: 91 US4.DIV
CURRENT FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR PELICATION NUMBER: US 09/924,340

PRIOR PILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PELICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-06-29
PRIOR PELICATION NUMBER: US 60/203,277
PRIOR PELICATION NUMBER: US 60/203,574
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Tready, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim
FILLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
Query Match 63.5%; Score 33; DB 9; Length 478; Best Local Similarity 60.0%; Pred. No. 1.4e+02; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 9; Length 478; 60.0%; Pred. No. 1.4e+02; ive 1; Mismatches 3; Indels
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ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 184, Application US/09746783
Publication No. US20030044935A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
MCCOy, John M.
LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 60.0.
Best Local 6; Conservative
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STATE: MA
                                                                                                                                                                                                                                             239 EVAPAGASYN 248
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                                                                                                                                                                 2 EVVPXGMSYS 11
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; ORGANISM: Homo sapiens
US-09-992-600A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-09-746-783-184
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Gaps

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AFFILGANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. US20020150885Alel Fluorogenic or Fluorescent Reporter Molecule
TITLE OF INVENTION: No. US201508161 Fluorescence
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
TITLE REPERENCE: 1735.0290005
CURRENT APPLICATION NUMBER: US 60/061,582
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR APPLICATION NUMBER: US 60/168,888
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR FILING DATE: 1998-010-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR PLILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 32; DB 10; Length 254;
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OTHER INFORMATION: Xaa = any amino acid, unknown, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-778-927A-53; Sequence 53, Application US/09778927A; Patent No. US20020068342A1
                           Sequence 66, Application US/09947387;
Patent No. US20020150885A1
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
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ORGANISM: Homo sapiens
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US-09-947-387-66
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SEQ ID NO 53
LENGTH: 254
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Matches
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US-09-820-843A-26

Sequence 26, Application US/09820843A

Sequence 26, Application US/09820843A

Publication No. US20030039963A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COUNCIL OF Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915

CURRENT APPLICATION WIMBER: US/09/820,843A

CURRENT APPLICATION WIMBER: US/09/820,843A

SOFTWARE: PALENTE 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PALENTE PALENTE APPLICATION OF CANDIDATE PROTEI

CURRENT APPLICATION UNGER: US/09/820,843A

SOFTWARE: PALENTE 2001-03-30

SOFTWARE: PALENTE PALENTE APPLICATION OF CANDIDATE PROTEI

LENGTH: 653
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                                                                                                       APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.095.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PAPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-09-06
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-25
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OTHER INFORMATION: iron(III) ABC transporter, permease protein

NAME/KEY: misc_feature

NAME/KEY: misc_feature

1 OTHER INFORMATION: gi|9654609

US-09-820-843A-26
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                                 Sequence 108, Application US/10000986 Publication No. US20030096247A1 GENERAL INFORMATION:
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 108
LENGTH: 478
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Sequence 4, Application US/10024066
; Sequence 4, Application US/10024066
; Patent No. US20020166134A1
; GENREAL INFORMATION:
; APPLICANT: Field, Loren J.
; APPLICANT: Field, Loren J.
; APPLICANT: Field, MUNENTION: CARDIOWYCCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
; TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
; FILE REPERENCE: 7037-450
; CURRENT APPLICATION NUMBER: US/10/24,066
; CURRENT FILING DATE: 2001-12-18
; PRIOR PAPLICATION NUMBER: PCT/US00/16827
; PRIOR PILING DATE: 2000-06-19
; RIOR PILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
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APPLICANT: Fasumarthi, Kishore Babu S.
APPLICANT: Pasumarthi, Kishore Babu S.
TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: AND METHORS FOR PREPARING AND USING SAME
FILE REPREBRUE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 1999-06-18
PRIOR PILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATCHIN VET. 2.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 32; DB 9; Length 289; 60.0%; Pred. No. 1.3e+02; tive 1; Mismatches 3; Indels
Pred. No. 1.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                      ; Sequence 2, Application US/10024066; Patent No. US20020166134A1; GENERAL INFORMATION:
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
  Best Local Similarity 60.0
Matches 6; Conservative
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                                                                   1 EEVVPXGMSY 10
                                                                                                             74 EEVFPLAMNY 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Mus musculus
US-10-024-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 289
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US-10-024-066-4
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US-10-024-066-2
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Search completed: June 4, 2003, 13:30:38
Job time: 15.25 secs
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4, 2003, 13:09:19 ; Search time 9.75 Seconds (without alignments) 33.195 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                        - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                 Scoring table:
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1: /cgn2_6/prcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Appl	5, App	5, App	5, App	i.	5177197	177197	, Appl	, Appl	, Appl	, Appl	Appli	Appli	Appli	Appli		, Appl		, Appl					Appli	Appli	
	ion			e 236,			No. 5	No. 5	9	99 a	φ	N	e 4,	e 4,	е 4,	e 7,	e 21						e 22,		, e	, e e	,
	Description	Seguence	Sequence	Sequence	Sequence	Patent No	Patent N		Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Sequence	00000
SOUTHER	ΠD	US-09-228-986-73	US-08-637-759B-236	8	US-09-201-945-236	5177197-51	5177197-1	5177197-30	US-09-357-952-66	US-09-521-650-66	US-09-168-888-66	US-08-580-988A-23	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22	US-08-464-517-6	US-08-463-772-6	* *175 785 00 011
	DB	4	7	m	4	Q	9	9	4	4	4	~	• •					7	m	ស	~	N	m	Ŋ	~	ო	•
	Length	947	45	45	45	65	410	1394	10	10	10	102	152	152	152	173	189	189	189	189	236	236	236	236	280	280	000
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	Score	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	C
	Result No.	-	2	m	. 4	ı.	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	,

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Sequence 73, Application US/09228986
Sequence 73, Application US/09228986
Sequence 73, Application US/09228986
September 100: 6359198
September 100: 6359198
September 100: 6359198
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: MAT Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FRASESQ for Windows Version 3.0
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                                                                                    Sequence 23, Appl
Sequence 23, Appl
Sequence 8, Appl
Sequence 8, Appli
Sequence 2, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 20, Appli
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Appli
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Sequence 2, A
Sequence 2, A
Sequence 8, A
         Sequence
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STATE: Georgia
COUWTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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; Patent No. 5876931
; GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patraa L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
PCT-US93-05000-6
US-08-46-517-23
US-08-246-361A-6
US-08-246-361A-23
US-08-463-772-23
US-07-947-120-8
US-08-472-893A-8
US-08-472-893A-8
US-08-464-517-20
US-08-464-517-20
US-08-464-517-20
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US-08-463-772-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.4%; Score 34; DB 4;
66.7%; Pred. No. 1e+02;
7ative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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Best Local Similarity 66...
6; Conservative
         ; ORGANISM: Pinus radiata
US-09-228-986-73
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LENGTH: 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                          RESULT 4
US-09-201-945-236
Sequence 236, Application US/09201945
Fatent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
ITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STRRET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REPERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
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TELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 45 amino acids
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                      STRANDEDNESS: single
TOPOLOGY: linear
                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                        1 EEVVPXGMSY 10
                                                                                                                                                                                                                                          1 EEISPLGWSY 10
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       amino acid
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Best Local Similarity
Matches 6; Conserv?
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STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                               US-08-871-355A-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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5177197-51
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Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
             APPLICATION NUMBER: US/08/637,759B
FILING DATE: U3-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCEY/DOCKET NUMBER: 31,284
FEFERENCEY/DOCKET NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
ITELEPROMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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NO
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                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
US-08-637-759B-236
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61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.5; tive 3; Mismatches 2; Indels
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                                        ; Sequence 66, Application US/09357952; Patent No. 6248904
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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                                                                                   GENERAL INFORMATION:
RESULT 8
US-09-357-952-66
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PAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENA; HELDIN, CARL-HENRIN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, TITLE OF INVENTIONS: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA;
                  APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
;MERNSTEDI, CHRISTER,HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
;LIA,HELDIN, CARL-HENRIK
;TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
;HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
;NUMBER OF SEQUENCES: 53
;CURRENT APPLICATION DATA;
;APPLICATION NUMBER: US/07/487,343
;FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Patent No. 5177197; ANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; HARNIEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH; LENA; HELDIN, CARL-HENRIK; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 6; Length 410;
Pred. No. 63;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                       63.5%; Score 33; DB 6; Length 65; 45.5%; Pred. No. 7.8;
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                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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Best Local Similarity
Matches 5; Conserv
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    Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 410
                                                                                                                                                                                                                                      ; LENGTH: 65
5177197-51
                                                                                                                                                                                                                      SEQ ID NO:51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5177197-30
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5177197-1
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5177197-1
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APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, Proteases
TITLE OF INVENTION: Cher Enzymes and the Use Thereof
TITLE OF INVENTION Other Enzymes and the Use Thereof
TITLE OF INVENTION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER PILING DATE: 21-JUJ-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Carana, John A.
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: No. Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
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US-09-521-650-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 4; Length 10; Pred. No. 1.5;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694 FILING DATE: 02-UUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
GENERAL TATLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.5%; Score 32; DB 60.0%; Pred. No. 21; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: McConathy, Evelyn H.
RECISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEPAX. 202-371-2540
TELEPAX. SEQUENCE CHARACTERISTICS:
                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
RELECOMMUNICATION INFORMATION:
TELECHONE: 713-777-2321
TELEPHONE: 713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                              TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-460-694-4
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  CLASSIFICATION: 424
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                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
TITLE OF INVENTION: No. 6345411el Fluorogenic or Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION NUMBER: US, 60/061, 582
CURRENT FILING DATE: 1998-10-10
EARLIER APPLICATION NUMBER: US, 60/061, 582
EARLIER APPLICATION NUMBER: US, 60/061, 582
EARLIER PILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
    Gaps
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  2; Indels
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  3; Mismatches
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OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/08580988A
Patent No. 5856161
                                                                                                                                                          RESULT 10
US-09-168-888-66
; Sequence 66, Application US/09168888
; Patent No. 6342611
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Best Local Similarity 50.0
Matches 5; Conservative
5; Conservative
                                             1 EEVVPXGMSY 10
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Matches
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: 173 amino acids
amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMSY 10
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; Sequence 4, Application US/08460744
; Sequence 4, Application US/08460744
; GENERAL INFORMATION:
; APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its CDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS: 8
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Wanhington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%; Score 32; DB 3; Length 152; 60.0%; Pred. No. 33;
Query Match 61.5%; Score 32; DB 2; Length 152; Best Local Similarity 60.0%; Pred. No. 33; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/07667711B
Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 11100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUDNIKK: USA

CIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,744

FILING DATE: 02-JUN-1995

CLASSIPICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MCCOnathy, Evelyn H.

REGISTRATION NUMBER: 35,279

REPERENCE/DOCKET NUMBER: 0609.4070005

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0%
...rhes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMSY 10
                                                                                     1 EEVVPXGMSY 10
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                                                                                                                               20 EEVFPLAMNY 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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COMPUTER IN PROCEED FORM

COMPUTER IN PROCESSION

CONFIDENT IN PROCESSION

CONFIDENT SPECIAL IN PROCESSION

CONFIDENT SPECIAL IN PROCESSION

CONFIDENT SPECIAL IN PROCESSION

CONFIDENT SPECIAL IN PROCESSION

APPLICATION NUMBER: 105/07/667,7118

FELLENOM: (202) 311-240

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-193-977-7

Query Match
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps
Qy 1 EEVVPXGMSY 10
Db 55 EEVFPLAMNY 64

Search completed: June 4, 2003, 13:14:58
Job time: 9.75 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

June 4, 2003, 13:04:09 ; Search time 28.25 Seconds Run on:

(without alignments) 51.885 Million cell updates/sec

AUDET-909-2 56

1 eevvpxgmhys 11 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 101002:* .: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980. :: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.

/ SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDS2/gcgdata/geneseqg-embl/AA1988.DAT:* | SIDS2|gcgdata|geneseq|geneseqp-embl/AA1989.DAT.|
SIDS2	gcgdata	geneseq	geneseqp-embl/AA1990.DAT.
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SIDS2	gcgdata	geneseq	geneseqp-embl/AA1992.DAT.
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SIDS2	gcgdata	geneseq	geneseqp-embl/AA1994.DAT.
SIDS2	gcgdata	geneseq	geneseqp-embl/AA1994.DAT.

/gcgdata/geneseq/geneseqp-embl/AA1996.DAT: /gcgdata/geneseq/geneseqp-embl/AA1997.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT: 'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:

SIDS2

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Description	Henatitis C virus		Hepatitis C virus							
ΙD	ABB80523	ABB80527	ABB80558	ABB80560	ABB80537	ABB80541	ABB80546	ABB80550	ABB80554	ABB80555
DB	23	53	23	23	23	23	23	23	23	23
% Query Match Length DB	11	11	11	11	11	11	11	11	11	11
% Query Match	96.4	96.4	96.4	96.4	87.5	87.5	85.7	85.7	85.7	85.7
Score	54	5.4	54	54	49	49	48	48	48	48
Result /No.	+	0	m	4		φ	7	ω	o,	1.0
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Hepatitis C virus Hepatitis C virus	itis C	tis C	tis C	itis C	is C	itis C	itis C	itis C	itis C	itis C	itis	itis C	itis C v	itis C	itis C	itis C	itis																
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11 46 82.1 12 46 82.1	45 80.	4 45 80	5 45 80.	6 45 80.	7 45 80.	8 45 80	45 80.	0 45 80.	1 45 80.	2 45 80.	3 45 80.	4 45 80	5 45 80.	45 80.	7 45 80.	45 80.	9 40 71.	0 40 71.	1 40 71.	2 40 71.	3 40 71.	4 40 71.	5 40 71.	6 39 69.	7 39 69.	8 39 69.	39 69.	.69 88 69.	1 39 69.	2 39 69.	3 39 69.	4 39 69.	39 69.

#### ALIGNMENTS

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
                                                                                                                                                          note= "N-terminal acetyl"
                                                                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                                                                                                                       note= "D-form residue"
                                                                                                                                       Location/Qualifiers
RESULT 1
ABB80523
ID ABB80523 standard; peptide; 11 AA.
                                                       08-OCT-2002 (first entry)
                                                                                                                                                                                               Misc-difference
                                                                                                                                          Key
Modified-site
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                                                                                                                        Synthetic.
                                      ABB80523;
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activity useful for treating disorders associated with hepatitis
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                                                                                                                                                                                   1 EEVVPXGMHYS
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                                                                                                                                                      Best Local Similarity
                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus protease
           virus protease
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                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                            Sequence
                                                                                                                                             Query Match
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                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory
                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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                                                                                                                                                                                                                      96.4%; Score 54; DB 23; Length 11; 100.0%; Pred. No. 0.00045; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-terminal acetyl"
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/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residue 7"
                             Brunck TK;
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                                                                                                      Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                             ABB80527 standard; peptide; 11
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                                                                                                                                                                                                                                          Conservative
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          (CORV-) CORVAS INT INC.
                             Levy OE,
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                                                                                                                                                                                                                                                           1 EEVVPXGMHYS
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                                               WPI; 2002-361643/39
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                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                    11 AA;
                                                                                    virus protease
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                            Lim-wilby M,
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                                                                                            hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                   The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38
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                                                                                                                                                                                                                                                                                                                                                                                                            96.4%; Score 54; DB 23; Length 11;
100.0%; Pred. No. 0.00045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80558 standard; peptide; 11 AA.
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Claim 17; Page 64; 69pp; English
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Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                               Similarity
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              11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         "Norvalyl carbonyl forming keto-amide linkage with residue 7"
virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
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                                                                             96.4%; Score 54; DB 23; Length 11;
100.0%; Pred. No. 0.00045;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                              ABB80560 standard; peptide; 11 AA.
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                                                                                                        11; Conservative
                                                                                                                               1 EEVVPXGMHYS 11
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                                                                                  Query Match
Best Local Similarity
                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                      virucide.
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                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
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                              Length 11;
Score 54; DB 23; Lengtn 11.
Pred. No. 0.00045;
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Pred. No. 0.0043;
          96.4%; Scor.
100.0%; Pred. No. v.
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                        ABB80537 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 64; 69pp; English.
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90.9%;
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ABB8054

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/note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibito activity useful for treating disorders associated with hepatitis
                                                                                                                                                                                                           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                         11
/note= "C-terminal amide"
                                                                                                                                                                            Location/Qualifiers
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                                    (first entry)
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nes 10; Conserv
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                                                                                                                                                                                            Modified-site
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                                  08-OCT-2002
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                                                                                                                                             Synthetic
    ABB80546;
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                                                                                                                                                                                                                                                                                                                                                               /note= "Norvalyl_carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                       Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21
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Pred. No. 0.0043;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                             'note= "D-form residue"
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                                                                                           ABB80541 standard; peptide; 11 AA.
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90.9%;
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Matches 10; Conservative
EEVVPXGQHYS 11
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                                                                                                                           ABB80541;
                                                                                                                                                                                                                                       virucide.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30.
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Pred. No. 0.0067;
0; Mismatches 1; Indels
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RESULT 7 ABB80546 ID ABB8

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08-OCT-2002
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                                                                                                                   "Norvaly1 carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                     'note= "N-terminal acetyl"
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                         Location/Qualifiers
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nes 10; Conservative
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                                                                                                                        /note=
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35.
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                                                        /note= "C-terminal amide"
/note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 65; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                CORV-) CORVAS INT INC
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WPI; 2002-361643/39.
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                                     virus protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease -
                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11
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                                                                                                                                                                                                                                                   85.7%; Score 48; DB 23; Length 11; 90.9%; Pred. No. 0.0067; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
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/note= "C-terminal amide"
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                                                                      Brunck TK;
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                                                                                                                                          Claim 17; Page 65; 69pp; English.
                 19-JUL-2001; 2001WO-US23169.
                                  21-JUL-2000; 2000US-220101P.
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                                                                                                                                                                                                                                                                     Conservative
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                                                                      Levy OE,
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                                                   (CORV-) CORVAS INT INC
                                                                                       WPI; 2002-361643/39
                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                         virus protease
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                                                                    Lim-wilby M,
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31-JAN-2002
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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nes 10; Conservative
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            hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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 compound of the invention having
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Pred. No. 0.017;
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sequence represents a peptide
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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/note= "
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Pred. No. 0.026;
0; Mismatches 1; Indels
80.4%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.026;
                           1; Indels
                           0; Mismatches
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                                                                                EEVVPXGMSYS
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  Query Match
                                                                                                                          RESULT 14
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/note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
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                                                                      ABB80524 standard; peptide; 11 AA.
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Best Local Similarity
Matches 10; Conservat
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Modified-site
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                                                                                                                                                                                                        08-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                        ABB80524;
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RESULT 15
ABB80524
ID ABB80524
ID ABB80524
AC ABB80
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DY 08-OC'
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Gaps

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10; Conservative 1 EEVVPXGMHYS 11 1 EEVVPXGMDYS 11

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Search completed: June 4, 2003, 13:11:13 Job time: 29.25 secs

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June 4, 2003, 13:07:09; Search time 22.5 Seconds (without alignments) 100.734 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
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sp_human:*
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sp_phage:*
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Maximum DB seq length: 200000000
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1 eevvpxgmhys 11
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

· D	Description	Q8rq86 fusobacteri	09x2e2 thermotoga	O9hlh8 thermoplasm		046486 corynebacte	O8ywp1 anabaena sp	Q9avk4 pisum sativ	Q57489 bacteroides	Q9pc35 xylella fas	Q40479 nicotiana t	Q91w50 nicotiana s	Q38317 lactobacill	Q9xvk4 caenorhabdi	Q9sa71 arabidopsis	Q8tz07 methanopyru	O27902 methanobact
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SON	Ð	 Q8RG86	Q9X2E2	оэнгне	<b>099UR5</b>	046486	Q8YWP	Q9AVK	057489	Q9PC35	04047	Q9LW5	038317	Q9XVK4	Q9SA71	Q8TZ07	027902
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	% Query Match Length DB	1063	308	322	1057	208	252	819	139	156	233	237	317	425	510	2042	264
	% Query Match	67.9	66.1	66.1	66.1	64.3	64.3	64.3	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	60.7
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or on ac e	O9pkh7 chlamydia m O84218 chlamydia t O84218 chlamydia t O29966 archaeoglob O9wcw0 avian infec Q9qgta avian infec Q9qgt1 avian infec
098XN9 098HU6 098KW92 09XAM3 027679 09KBA1 09612 09612 098Y11 099Y016 09Y011 09Y011 09Y011 09Y011 09Y011 09Y011 09H019 09H019	09PKH7 084218 084218 09WCW0 09T025 09QGT4 09QGT3
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### ALIGNMENTS

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The SEQUENCE FROM N. A. SEGUENCE FROM N. A. SEQUENCE FROM N. A. Bartman A. Grechkin G., Los T., Lykidis A., Bartman A., Bartman A., Grechkin G., Zhu L., Bartacharyya A., Bartman A., Gardner W., Greckhin G., Zhu L., A Usieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., A Larsen M., Kyrpides N., Overbeek R., Tenstein M., Kyrpides N., Overbeek R., Genome sequence and analysis of the oral bacterium Fusobacterium RI. Dascone sequence and analysis of the oral bacterium Fusobacterium RI. Dasceriol. 184:2005-2018 (2002).

R. Bartis Abolo554; AAL94625.1; -. REMBL; ABOLO554; AAL94625.1; -. REMBL; ABOLO554; AAL94625.1; -. SeQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                      01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last amnotation update)
Carbamoyl-phosphate synthase large chain (RC 6.3.5.5).
                                                                                                                                                                     Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                      PRT; 1063 AA
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Matches 6; Conservative
                                    PRELIMINARY;
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195 EIVPNGLNYS 204
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                                    Q8RG86
RESULT 1
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RESULT Q9X2E2 audet-909-2.rspt

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EMBL; AP003361; BABS7365.1; -. EMBL; AP003132; BAB42298.1; -. HSSP; P00968; ICS0.
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus.
NCBI_TaxID=158878, 158879;
                                6; Conservative
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190 EIVSNGLHYS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
                                                                                              3 VVPXGMHY 10
                                                                                                                                                         66 WVPDGLHY 73
   Best Local Similarity
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                             Matches
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Q99UR5
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STRAIN=MBBB / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg S.L., Smith H.O., Venter J.C., Fraser C.M., White O.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
Genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                       Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.1%; Score 37; DB 16; Length 308; 75.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoplasma acidophilum.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease, Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJN-2001 (TrEMBLrel. 17, Last annotation update)
Glucose-fructose oxidoreductase related protein.
                                                                                              , Last sequence update)
, Last annotation update)
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      308 AA
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                                                                                                                                                         protease activity modulator HFLK
                                                                 Created)
      PRT;
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EMBL, AL445063; CAC11395.1; -.
InterPro; IPR000683; GFO_IDH_MocA.
Pfam; PF01408; GFO_IDH_MocA; 1.
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MEDLINE-20479972; PubMed=11029001;
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InterPro; IPR001310; GED.
InterPro; IPR001972; Stomatin.
Pfam; PP01145; Band 7; 1.
SMART; SM03021; STÖMATIN.
SMART; SM03022; GED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001819; AAD36885.1; -.
                                                          01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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   PRELIMINARY;
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41 VVPSGIHY 48
                                                                                                                                                                                                                          Thermotoga maritima.
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SEQUENCE 322 AA;
                                                                                                                                                                                                                                                          Bacteria, Thermot
NCBI_TaxID=2336;
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SEQUENCE FROM N.A.

SPECIES=S. aureus (strain Mu50), and S.aureus (strain N315);

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito. T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizucani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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  1; Indels
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                                                                                                                                                                                                                                                                                                              01-UN-2001 (TrEMBLrel. 17, Created)
01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Carbamoyl-phosphate synthase large chain.
PYRAB OR SAN1203 OR SA1046.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00098; CPSASE.

PROSITE; PS00866; CPSASE_1; 2.

PROSITE; PS00867; CPSASE_2; UNKNOWN_2.

PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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1; Mismatches
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InterPro; IPR004362; MGS_like.
InterPro; IPR000169; SHprot acsite.
Pfam; PP02189; CPSase_LchaIn; 2.
Pfam; PP02786; CPSase_LD2; 2.
Pfam; PP02787; CPSase_LD3; 1.
Pfam; PF02142; MGS; 1.
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1D Q46486
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01-JUN-2001
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                                                                                                           Q9AVK4;
                                                                         Q9AVK4
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RESULT 7
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                                      Q9AVK4
                                                                                SOCCOS REPLACED BY THE PROPERTY OF THE PROPERT
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SPECIES=C.striatum; STRAIN=M82B;

MEDLINE=20194806; PubMed=10732668;

Tauch A., Krieft S., Kalinowski J., Puhler A.;

"The 51,409-bp R-plasmid pTP10 from the multiresistant clinical isolate Corynebacterium striatum M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human pathogens.";
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                                                                                                                                                                                                                    SPECIES=C.xerosis; STRAIN=M82B;
MEDLINE=96117603; PubMed=8559800;
Tauch A., Kasing F., Kalinowski J., Puhler A.;
Tauch A., Kasing R. xerosis composite transposon Th5432 consists of
two identical insertion sequences, designated IS1249, flanking the
erythromycin resistance gene ermCX.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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   Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;
                                      Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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EMBL, AP003586; BAB77929.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 252 AA; 28831 MW; 925572DASDICA519 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Alr1563.
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Best Local Similarity 50.0
Matches 5; Conservative
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Matches 5; Conservative
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235 EMIVPAGLHF 244
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130 DVIPEGKHYA 139
                                                                                                           NCBI_TaxID=1725, 43770;
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MEDLINE=21231727; PubMed=11333309;
Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;
"The Molecular Characterization and in situ Expression Pattern of Pea
SCARECROW Gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A multiple site-specific DNA-inversion model for the control of Ompi
phase and antigenic variation in Dichelobacter nodosus.";
Mol. Microbiol. 17:183-196(1995).
                                                                                                                                  Pisum sativum (Garden pea).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
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MEDLINE=96020672; PubMed=7476204;
Moses E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
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MEDLINE-86557263, PubMed=8654969;
Billington S.J., Sinistaj M., Cheetham B.F., Ayres A., Moses E.K., Katz M.E., Rood J.I.;
Tidentification of a native Dichelobacter nodosus plasmid and implications for the evolution of the vap regions.";
Gene 172:111-116(1996).
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01-DEC-2001 (TERMELE). 01, Last sequence update)
01-DEC-2001 (TERMELE). 19, Last annotation update)
DAA ligase (Fragment).
BACTEROIDES DOGOUS (Dichelobacter nodosus).
Bacteria, Proteobacteria, gamma subdivision, Cardiobacteriaceae,
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PROSITE; PS00588; FLAGELLA BB_ROD; UNKNOWN 1.
SEQUENCE 819 AA; 90372 Ww; 41B67Bb6DC7ZADFA CRC64;
                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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819 AA.
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EMBL, AB0484713; BABS3155.1; -.
InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR005202; GRAS.
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                                          Created)
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InterPro, IPR001357, BRCT.
Ffam, PF00533, BRCT; 1.
SMART, SM00292, BRCT; 1.
PROSITE, PS50172; BRCT; 1.
                                          (TrEMBLrel. 17,
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  PRELIMINARY;
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PRELIMINARY;
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RA ALVAREDRA A.J.G., Reinach F.C., Arruda P., Abreu F.A., Baptiera C.S.,
ALVARDANINE-20365117; PubMed=10910347;
RA ALVAREDRA A.J.G., Reinach F.C., Arruda J.B., Babtiera C.S.,
BARTOS M.H., Bonacocroit E.D., Bordin S., Bove J.M., Eriones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C., M.,
RA Coutinho L.L., Cristofani M.D. Dias-Freto B. P., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Lopes C.R., Machado J.A.,
RA Homos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Rachado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques N.V., Martins E.A., Martins E.M.F., Matsukuma A.Y.,
Manck C.F.M., Miracca B.C., Munget E.L., Oliveira M.P., Perquero J.B.,
A honni A. Jr., Nobrega F.G., Nunse, Palmieri D.A., Paris A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A de Silveira J.F., Silvestri M.L., Sawasaki H.E.,
A da Silve A.C.R., da Silva A.M., da Silva M.J., Ge Souza A.J.,
A de Souza A.D., Terenzi M.F., Santelli R.V., Sawasaki H.E.,
A da Silva A.C.R., da Salva A.M., da Silva M.J., Teraboto M.H.,
A de Souza A.D., Terenzi M.F., Silveira W.J., de Souza A.D.,
A de Souza A.D., Terenzi M.F., Silveira W.J., de Souza A.D.,
A de Souza A.D., Terenzi M.F., Salveiral J.C.;
A Sago M.A., Zatonali S., Stubal J.C.;
A Sago M.A., Satubal J.C.;
A Salveira A.D., Terenzi M.F., Salveira M.J.,
A Sago M.A., Satubal J.C.;
A Sago M.A., Satubal J.C.;
A Sago M.A., Satubal J.C.;
A Salveira A.D., Terenzi M., Satubal J.C.;
A Sago M.A., Satubal J.C.;
A Sago M.A.
                                                                                 Gaps
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Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                  Query Match 62.5%; Score 35; DB 2; Length 139; Best Local Similarity 55.6%; Pred. No. 24; Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
  139 AA; 15052 MW; E0E110AA4B7D4708 CRC64;
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Hypothetical protein; Complete proteome.
SEQUENCE 156 AA; 17144 MW; D8358619C6671A5D CRC64;
                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf1950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE004014; AAF84752.1; -. InterPro; IPR002545; CheW.
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es 5; Conservative
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                                                                                                                3 VVPXGMHYS 11
                                                                                                                                         1 | | | | 21 IVPAGVHWS 29
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SEQUENCE
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EMBL; ABO16264; BAA97122.1; -.
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                                                                                              Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Bepmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                             STRAIN=BY4; TISSUE=LEAF;
MEDLINE=95276459; PubMed=7756828;
Ohme-Takagi M., Shinshi H.;
"Ethylene-inducible DNA binding proteins that interact with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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              vi-NVV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) EREBP-2.
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Last annotation update)
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01-0cT-2000 (TrEMBLrel. 15, Last sequence up
01-0cT-2002 (TrEMBLrel. 21, Last annotation
Ethylene-responsive element binding factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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01-NOV 1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
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                                                                              Nicotiana tabacum (Common tobacco).
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MEDLINE=20399450; PubMed=10945353;
                                                                                                                                                                                                                                                                                            ethylene responsive element.";
Planc Cell 7:13-182(1995).
EMBL; D38126; BAA07324.1; -.
HSSP; 080337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00847; AP2-domaIn; 1.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TF_AP2; 1.
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ProDom; PD001423; TF AP2; 1.
SMART; SM00380; AP2; 1.
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Pfam; PF00847; AP2-domain; 1.
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Best Local Similarity 60.0.
Best Local 6; Conservative
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1 EEVVPXGMHY 10

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119 EEILPOGVH 127

RESULT 10

040479

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investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81109; CAB03241.1; -.
InterPro; IPR000719; Euk pkinase.
                                                                                                                           MEDLINE=99069613; PubMed=9851916;
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Matches 6; Conserv
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                                             NCBI_TaxID=6239;
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Q8TZ07
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MEDLINE=93231538; PubMed=8472961;
Fremaux C., De Antoni G., Raya R., Klaenhammer T.;
Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Engel G., Altermann E., Klein J., Henrich B.; "Structure of a genome region of the Lactobacillus gasseri temperate phage phi adh covering a repressor gene and cognate promoters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Altermann E., Klein J., Henrich B.;
Pyrimary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh.";
Gene 236:333-346(1999).
                                                                                                                                                                                                                                                                                                                                      MEDLINE=55138034; PubMed=7836307;
Henrich B., Binishofer B., Blaesi U.;
"Primary structure and functional analysis of the lysis genes of
Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
                                                                                                                                                 Lactobacillus bacteriophage phi adh.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=12417;
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                                                                                                                                                                                                                         Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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CE 317 AA; 34703 MW; 9FF2715EE43561C7 CRC64;
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Last annotation update)
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EMBL, AJ131519; CAB52540.1; -
Interpro; IPR002053; GH 25.

Interpro; IPR003646; SH3 bac.

Pfam; PF01183; Glyco hydro 25; 1.

ProDom; PD004620; GH 25; 1.
                                                                    PRT;
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                                                                   PRELIMINARY;
                                                                                         01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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94 QAVVPKGRHY 103
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Gene 126:61-66(1993).
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Matches 6; Conserv
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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60.0%; Pred. No. 92;
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                                                                                                                                                                                                                                                            Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                Percy C.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09SA71;
0-NAX-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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ProDom; PD000001; Euk_pkinase; 1.
PROSTTE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
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Arabidopsis thaliana (Mouse-ear cress).
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DG 08TZ07; PRELIMINARY; PRT; 2042 AA.

CQ 08TZ07;
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein of the CobN/Mg-chelatase family.

MC0134.

SM Chancopyrus kandleri.

OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.

OX NCBL_TaxID=2320;
RN SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA SEARCH A.1. Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA SLEARIS-1927647; PubMed=11930019;
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Malykh A.G., Roonin E.V., Kozyavkin S.A.;
RA Malykh A.G., Roonin E.V., Kozyavkin S.A.;
RA Malykh A.G., Roonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RD Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

RE EMBL; AE010313; AAM01351.1; -.

OLDETY Match

OLDETY Match

SC COMPLETE DOLOGE STATIS MW; 8386E092A62C112A CRC64;

OLDETY Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Search completed: June 4, 2003, 13:13:25 Job time: 24.5 secs

924 EVVPIGLH 931

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:04:34; Search time 6.25 Seconds (without alignments) 72.998 Million cell updates/sec Run on:

AUDET-909-2 56 1 eevvpxgmhys 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMADIES

		d			SUMMARIES		
Result		Query					
No.	Score		Length	DB	D	Description	ption
Н	38	7	10		RB FUS	08rg86	
7	37	66.1	1057	٦	CARB_STAAM	099ur5	
m	37	66.1	1057	Н	CARB_STAAW	P58940	
4	36	64.3	102	Н	Y11K_TYDVA	P31619	
S	36	4.	460	П	UME1_YEAST	003010	
9	36	4.	743	7	YK47 YEAST	P36148	
7	35	62.5	227	Н	IDII_MESAU	035586	
80	35	ď	308	7	GAAB_METTH	026806	
Ø	34	ö	426	П	SLS1_YARLI	099158	
10	33	58.9	513	Н	PHSL_DESBA	P13065	
11	33	æ.	627	7	MUTL_BACSU	P49850	
12	33	æ.	1188	П	KPBA_CAEEL	P34335	caenorhabdi
13	33	58.9	1396	Н	VLTF_BPT5	P13390	_
14	32	57.1	126	Н	TKNK_BOVIN	P08858	
15	32	7	267	Н	RR2 CHLVU	P56351	
16	32	~	288	Н		004827	
	32	2	289	Н	CGD2_HUMAN	P30279	homo sapien
	32	^	289	Н		P30280	
	32	7	291	Н	CGD1_BRARE	090459	
	32	~	291	Н		P50755	xenopu
	32	^	291	Н	CGD2_CHICK	P49706	_
	32	57.1	291	Н	CGD2_XENLA	P53782	xenopus
	32	7	292	-	CGD1_CHICK	P55169	gallu
	32	_	292	Н	CGD3_HUMAN	P30281	homo
	32	7.	295	Н	CGD1_HUMAN	P24385	homod
	32	۲.	295			P25322	mus n
	32	57.1	295	Н	CGD1_RAT	94	rattus norv
	32	ζ.	341	Н	HYPE_AZOVI	P40595	azotobacter
	32	57.1	353	Н		88	bacillus an
	32	57.1	759	Н	SCT1_YEAST	P32784	saccharomyc
31	32	57.1	877	Н		074377	schizosacch
	32	57.1	1401	Н		Q9kv29	vibrio chol
33	32	57.1	2717	Н	ZEP1 HUMAN	P15822	homo sapien

	P97885 rattus norv Q58349 methanococc				
CD22 HUMAN REV SIVCZ	SZO5 RAT Y939 METJA	YHAI CRYPA RL3_ARCFU	ALFE SHEEP Y325 HAEIN	ENP3_HUMAN PTBA_BACSU	DCMB_MOOTH ETR1_BRAOL
1	пп,				
847	130	319 331	363 450	529 609	674 735
56.2	55.4	55.4	55.4	55.4	55.4 55.4
31.5	31	31 31	31 31	31	31
6. 6. 4. 7.	36	დ თ უ ო	40 41	42	44 45

### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ľ
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lancet 357:1225-1240(2001).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP phosphate + L-glutamate + carbamoyl phosphate.

-!- COFACTOR: Binds three manganese ions (By similarity).
-!- PATHWAY: Arginine biosynthesis, first step.
-!- PATHWAY: Pyrimidine biosynthesis, first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=MUSO / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Oduchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Muzutan-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanchisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                   OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamotyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase amonia chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
             Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                         ATP-binding; Manganese; Complete proteome.
DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                    Score 38; DB 1; Length 1058;
                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                           1058 AA; 117451 MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus (strain Mu50 / ATCC 700699), and
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                             ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1057 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity). SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                   Pred. No. 10;
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 PS00867; CPSASE 2; 2
                                                                                                                                                                                                                                      67.98;
                                                                                                                                                                                                                                                   60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                Conservative
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190 EIVPNGLNYS 199
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PROSITE;
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NP_BIND
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METAL
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-1- PATHWAY: Pyrimidine biosynthesis; first step.
-1- SUBNUT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
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-!- CAPALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
-!- CAPALYTIC ACTIVITY: 2 ATP + L-glutamoyl phosphate.
-!- COFACTOR: Binds three manganese ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Samanoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
5-Zubamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)
CARB OR PYRAB OR MW1086.
                                                                                                                                                                                                                                                                                                                   PRINTS; PR00098; CPSASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
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SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 1057; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
MANGANESE I (BY SIMILARITY).
MANGANESE I AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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Bacteria, Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding, Manganese; Complete proteome.
                                                                                                    InterPro; IPR005479; CPase L D2.
InterPro; IPR005480; CPase L D3.
InterPro; IPR005481; CPase L N.
InterPro; IPR004362; MGS like.
Pfam; PF00289; CPSase L Chain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117171 MW;
EMBL; AP003361; BAB57365.1; -.
EMBL; AP003132; BAB42298.1; -.
HSSP; P00968; 1CSO.
                                                                                                                                                                                                            Pfam; PF00289; CPSase_L_Chain;
Pfam; PF02786; CPSase_L_D2; 2.
Pfam; PF02787; CPSase_L_D3; 1.
Pfam; PF02142; MGS; 1.
                                                                            interPro; IPR005483; CPase L.
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60.0%;
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les 6; Conservative
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546
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302 352
284 284
298 298
300 300
820 821
832 831
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SEQUENCE
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NP BIND
NP BIND
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102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
 SQ SEQUENCE
                          Query Match
                                                                                                                                       RESULT 5
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonous plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                   OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                         EMBL; AP004825; BAB94951.1; -.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese.
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                                                                                                                                                                                       CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 37; DB 1; Length 1057; 60.0%; Pred. No. 16; 2; Indels 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                           ALLOSTERIC DOMAIN
                                                                                                                                                                                                                                                              ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
  -!- SIMILARITY: BELONGS TO THE CARB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92188538; PubMed=1546458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A42452; A42452.
InterProv; IPRO05621; Gemini mov.
Pfam; PP01708; Gemini mov; I.
Hypothetical protein.
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1057
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1057 AA;
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Matches 6; Conserv
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P31619;
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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RC SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=5288C / AB972;

RX MEDLINE=97131271; PubMed=9169875;

RX BUSSEY H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Araujo R., Churcher C.M., Coster F., Davis K., Davis R.W., Cherry J.M., A Dietrich F.S., Delius H., Diraclo T., Dubois E., Duesterhoeft A., Dietrich F.S., Delius H., Diraclo T., Dubois E., Duesterhoeft A., Dietrich F.S., Hebling U., Heumann K., Hilbert H., Hillier L., RA Hulicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Romp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., RAM Hall J., Mesenguy F., Mewes H.-W., Mirtipati S., Moestl D., RA Marathe R., Mesenguy F., Mewes H.-W., Mirtipati S., Moestl D., RA Marller-Auer S., Namath A., Nettwich U., Oefner P., Pearson D., RA Greens B., Schramm S., Schroeder M., Scharfe M., Schraff M., Schroeder M., Scharfe M., Schraff R., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Rim alsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Rim and S.C., Burnisky S., Vierendeels F., Vissers S., Namath R., Mannett E., Redlarion T.P., Ram The mucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

RT "The mucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

REGULATION TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILENCING. TO YEAST WITH AND WIM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                 Gaps
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                                                                                 .
0
Score 36; DB 1; Length 102;
Pred. No. 2.3;
                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A364A;
Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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ID UMEI YEAST

AC 003010; P87330;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 11-JUN-2002 (Rel. 41, Last annotation update)

DF 15-JUN-2002 (Rel. 41, Last annotation update)

DF 16-JUN-2002 (Rel. 41, Last annotation update)

DF 16-JUN-2002 (Rel. 41, Last annotation update)

DF 16-JUN-2002 (Rel. 41, Last annotation update)
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
SMART; SM00320; WD40; 3.
PROSITE; PS00678; WD REPEATS_1; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_2; FALSE_NEG.
                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMEI OR WIMS OR YPLISSC OR LPI7C.
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64.3%;
                                                                                     Conservative
                                                                                                                                                                  2 EVVPXGMHYS 11
                                                                                                                                                                                                                 :||| |::||
7 QVVPSGINYS 16
                                  Best_Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T04309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van Vliet-Recdijk J.C., Planta R.J.;
submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UTN-1994 (Rel. 29, Created)
01-UTN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCPI-MET1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 743;
Pred. No. 18;
                                                                                                                                                                                                                                     64.3%; Score 36; DB 1; Length 460; 62.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                         411 451 WD 4.
460 AA; 51022 MW; AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743 AA; 83644 MW; 84B9946E56B82F15 CRC64;
                                 Transcription regulation; Meiosis; Repeat; WD repeat.
PROSITE; PS50294; WD_REPEATS_REGION; FALSE_NEG.
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                             2; Mismatches
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InterPro; IPR002123; Acyltransferase.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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75.0%;
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                                                                                                                                                                                                                                                                 Local Similarity 62.5
les · 5; Conservative
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nes 6; Conservative
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379
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                                                                                  276
339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
YK47 YEAST
AC P36148;
DT D1-UJN-1994
DT 01-UJN-1994
DT 01-UJN-1994
DT 01-UJN-1994
DT 01-UJN-1994
DT 01-UJN-1994
DE Hypothetical
GN SACCHATOMYCEE
OC BACAPTOMYCEE
OC SACCHATOMYCEE
OC SACCHATOMYCEE
OC SACCHATOMYCEE
OC SACHATOMYCEE
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035586;
                                                                                                                                                                        SEQUENCE
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                                                                                     REPEAT
REPEAT
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ID IDII_ME
AC 035586;
DT 30-MAY-
DT 30-MAY-
DT 15-JUN-
                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97373600; PubMed=9228075;
Paton V.G., Shackelford J.E., Krisans S.K.;
Paton V.G., Shackelford J.E., Krisans S.K.;
"Cloning and subcellular localization of hamster and rat isopentenyl diphosphate dimethylallyl diphosphate isomerase. A PTS1 motif targets the enzyme to peroxisomes...;
J. Biol. Chem. 272:18945-18950(1997).
-! FUNCTION: CATALYZES THE 1,3 ALLYLIC REARRANGEMENT OF THE HOWOALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS HIGHLY ELECTROPHILIC ALLYLIC ISOMER, DIMETHYLALLYL DIPHOSPHATE (DMAPP).
sopentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase
                                                     Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PATHWAY: ISOPRENOID BIOSYNTHETIC PATHWAY WHOSE END PRODUCTS INCLUDE DOLICHOLS, UITAMINS A, D, E, AND K, STEROID HORMONES, CAROTENOIDS BILE ACIDS AND CHOLESTEROL.
-i- SUBCELLULAR LOCATION: Percoxisomal.
-i- SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE I FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0TDN-2002 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD004109; IPP isomerase; 1.
Isomerase; Isoprene blosynthesis; Cholesterol biosynthesis;
Sterol biosynthesis; Peroxisome; Magnesium.
ACT SITE 86 86 BY SIMILARITY.
ACT_SITE 148 148 BY SIMILABITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%; Score 35; DB 1; Length 227; 70.0%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
MICROBODY TARGETING SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 148 BY SIMILARITY.
225 227 MICROBODY TARGETING SIGNAL
227 AA; 26317 MW; F500A6586385E803 CRC64;
                (Isopentenyl pyrophosphate isomerase 1) (IPPI1).
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002667; IPP isomerase.
InterPro; IPR000086; NUDIX hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF003836; AAC53283.1; -.
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                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                      NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                  diphosphate.
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-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
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                                                                                                                                                                                                                                                     SEQUENCE
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P13065;
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
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                        Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harison D., Hang L., Kaagle P., Lumm W., Pothiers B., Qùu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum delah: functional analysis and comparative genomics."; J. Bacteriol. 197-7135-7155 (1997).

-! CATALYIC ACTIVITY: APP + xanthosine 5'-phosphate + L-glutamine + H(2)O = AMP + diphosphate + GMP + L-glutamate.

-! PATHWAY: GMP biosynthesis.

-! PATHWAY: GMP biosynthesis.

-! SUBUNIT: HETEROIMER COMPOSED OF A GLUTAMINE AMIDOTRANSFERASE SUBUNIT (B) (POTENITAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boisrame A., Beckerich J.-M., Gaillardin C.;
"Slaip, an endoplasmic reticulum component, is involved in the
protein translocation process in the yeast Yarrowia lipolytica.";
J. Biol. Chem. 271:11668-11675 (1996).
-!- FUNCTION: INVOLVED IN THE PROTEIN TRANSLOCATION PROCESS. MAY
INTERACT DIRECTLY WITH TRANSLOCATING POLYPEPTIDES TO FACILITATE
THEIR TRANSFER AND/OR HELP THEIR FOLDING IN THE ER. IT IS NOT
REQUIRED FOR VIABILITY BUT IS ESSENTIAL FOR OPTIMAL GROWTH AT
ELEVATED TEMPERATURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Dipodascaceae, Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR01674; GMP synt_C.
Pfam; PF00958; GMP synt_C; 1.
TIGRFAMs; TIGR00884; guaA_Cterm; 1.
Ligase; GMP blosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 1; Length 308; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMP-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND 29 35 ATP (BY SIMILARITY).
SEQUENCE 308 AA; 34403 MW; F2DCF6ED202CAECI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.6%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yarrowia lipolytica (Candida lipolytica).
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000850; AAB85215.1; ALT_INIT.
HSSP; P04079; 1GPM.
               MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 20460 / W29;
MEDLINE=96216076; Pubmed=8662639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 EEVVESGLHES 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLS1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
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Q99158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SLS1_YARLI
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01-JNN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (EC 1.18.99.1) (NiFeSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: HETERODIMER OF A LARGE AND A SWALL SUBUNIT.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- MISCELLANBOUS: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS ...
TRANSPORT VEHICLE FOR BOTH SUBUNITS.
-!- SIMILARITY: BELONGS TO THE [NIFE] / [NIFESE] HYDROGENASE LARGE SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The crystal structure of a reduced [NiFeSe] hydrogenase provides an image of the activated catalytic center.";

Structure 7:557-566(1999).

-!- CATALYTIC ACTIVITY: 2 reduced ferredoxin + 2 H(+) = 2 oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLS1 PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL).
, 0ACD7EF17540B8E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydrogenlyase large chain).
Desulfovibrio baculatus (Desulfomicrobium baculatus).
Bacteria; Proteobacteria; delta subdivision; Desulfomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garcin E., Vernede X., Hatchikian E.C., Volbeda A., Frey M., Fontecilla-Camps J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 26; 1; Indels Live 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ferredoxin + H(2).
-!- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Menon N.K., Pect H.D. Jr., le Gall J., Przybyla A.B.
J. Bacteriol. 170:4429-4429(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS). MEDLINE=99306038; Pubmed=10378275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                                                                                                                                                                                                                                                                                            InterPro, IPR000886; BR target. PROSTIE; PS00014; BR TARGET; 1. Endoplasmic reticulum; Signal. SIGMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 426 PI
426 AA; 47201 MW;
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Best Local Similarity 44.4°,
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                           EMBL; Z50154; CAA90516.1;
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A Zevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Rinseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Joris B., Karamata D., Kasahara Y., Klashch J., Harwood C.R., Henaut A.,
A Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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"Bacillus subtilis mutS mutL operon: identification, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                      PDB; 1CC1; 01-JUN-99.
InterPro; IPR001501; Ni hdL.
Pfam; PF00374; NiFeSe Hases; 1.
PROSITE; PS00500; NI HGENASE L 1; 1.
PROSITE; PS005008; NI HGENASE L 2; 1.
Oxidoreductase; Periplasmic; Nickel; Selenium; Selenocysteine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 513;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56683 MW; AC8285A6F80576FC CRC64;
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NICKEL.
IRON 1 AND NICKEL.
IRON 2.
NICKEL.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96349107; PubMed=8760914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbiology 142:2021-2029(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA mismatch repair protein mutl
                                                                                                                                                           EMBL; M18271; AAA23375.2; -.
PIR; A33101; HQDVLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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P49850;
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MUTL_BACSU
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Rieger M., Rivolta C., Rocha E., Rapoport G., Rey M., Reynolds S.,
Sato T., Scanlan E., Schleder B., Rose M., Sadaie Y.,
Sekguchi J., Sekowska A., Seroc S.J., Serror P., Shin B.S., Soldo B.,
Sekiguchi J., Sekowska A., Seroc S.J., Perror P., Shin B.S., Soldo B.,
A scheuchi M., Tamakas A., Tanaka T., Takahashi H., Takemaru K.,
Tosato V. Uchiyama S., Vandahol M., Vannier P., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamanoto H., Yamane K., Yasamoto K., Yata K.,
The complete genues sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                  NATURE 390, 249-256 (1997).

-I FUNCTION: THIS REPOTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN LEUKTION: THIS REPOTEIN IS INVOLVED IN THE REPOTEIN THAT REPORTS.

REPAIR. MAY ACT AS A "WOLECULAR MATCHMAKER", A PROTEIN THAT REPAIR. MAY HE FORMATION OF A STABLE COMPLEX BETWEST TWO OR MORE DNA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF BING PART OF A FINAL EFFECTOR COMPLEX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable phosphorylase B kinase alpha regulatory chain (Phosphorylase
kinase alpha subunit).
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteome. 70431 MW; 068A0509CC265343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00058; DNA MISMATCH_REPAIR_1; 1. DNA repair; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, U27343; AAB19236.1; --
EMBL, Z99112; CAB13578.1; --
HSSP, P23367; 1BKN.
Subtlists, BG11402; mutl.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; NNA mis_repair.
InterPro; IPR004359; HIS_KIN_sig.
Pfam; PF01119; DNA mis_repair.
Pfam; PF02119; HATPase_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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KPBA CAEEL
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RESULT 14
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             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Jones M., Kershaw J., Kirsten J., Hillier L., Jier M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownken R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PHOSPHORYLAE B KINASE CATALYZES THE PHOSPHORYLATION OF SERINE IN CERTAIN SUBSTRATES, INCLUDING TROPONIN I. THE ALPHA CHAIN MAY BIND CALMODULIN (BY SIMILARITY).
-!- PATHWAY: Glycogen metabolism.
-!- SIMILARITY: BELONGS TO THE PHOSPHORYLASE B KINASE REGULATORY CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                            "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage T5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Glycogen metabolism; Calmodulin-binding.
SEQUENCE 1188 AA; 135558 MW; DE9BB875F3603863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequence of the bacteriophage T5 ltf gene."; Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 1188;
Pred. No. 1.2e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaliman A.V.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1330, 048502, 01-330, 01-330, 01-330, 01-330, 01-330, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 01-320, 
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L15188; AAA27954.2; -. PIR; S44754; WormPep; C14B9.8; CE26870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      950 EEYAEDĞIHYS 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T5-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kryukov V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLTF BPT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The
FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLTF_BPTS
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                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGGGGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                           between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-!- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE POLYMANNOSE O ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                     MEDLINE-88289370; Pubbled=3267228;
Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nucleotide sequence of bacteriophage T5 DNA at the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 1396;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             986 986 V -> A (IN REF. 2).
1396 AA; 147989 MW; 18CD2192F65FFFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
10-NOV-1988 (Rel. 09, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 126 AA.
[3] PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, M14351; AAA30723.1; -.
EMBL, M14347; AAA30723.1; JOINED.
EMBL, M14448; AAA30723.1; JOINED.
EMBL; M14349; AAA30723.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AJ001191; CAA04591.1; -. PIR; S01982; S01982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X69460; CAA49220.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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P08858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S., Tsudzuki T., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T., Inamura A., Yoshinaga K., Sugiura M.; Hanzina M.; Hamada A., Ohta T., "Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly involved in Chloroplast division."; Proc. Natl. Acad. Sci. U.S., 94:5967-5972 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                               1 20 POTENTIAL.
21 83 NEUROKININ B.
99 126 AMIDATION (G-96 PROVIDE AMIDE GROUP).
126 AA; 13871 MW; 446EF433498EC059 CRC64;
                                                                                                                                                                                                                                                                                         .
0
               PIR; A25905; A35905.
InterPro; IPR003635; Neurokinin.
InterPro; IPR003640; Tachykinin.
ProDom; PD020370; Neurokinin; 1.
PROSTE; BS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%; Score 32; DB 1; Length 267; 40.0%; Pred. No. 40; tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                   57.1%; Score 32; DB 1; Length 126; 66.7%; Pred. No. 19; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein, Chloroplast.
SEQUENCE 267 AA; 30699 MW; 7903075340BD900F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Chloroplast 30S ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AB001684, BAA57862.1; -.
InterPro; IPR001865; Ribosomal S2.
Pfam; PR001818, Ribosomal S2; 1.
PIGNTS, PR00195; RIBOSOMĀLS2.
TIGREĀMS; TIGR01011; FPSB bact; 1.
PROSITE; PS00962; RIBOSOMĀL S2_1; FALSE_NEG.
PROSITE; PS00963; RIBOSOMĀL S2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=IAM C-27 / Tamiya;
MEDLINE=97303241; PubMed=9159184;
EMBL; M14350; AAA30723.1; JOINED.
                                                                                                                                                                                                                                                                    Local Similarity 66.7
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                     28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMH 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorella vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                      RR2_CHLVU
P56351;
                                                                                                                                                                                                  MOD RES
SEQUENCE
                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                  PEPTIDE
                                                                                                                                   SIGNAL
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Matches
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ID_RR2_C
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Gaps

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2; Indels

Conservative

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Search completed: June 4, 2003, 13:11:45
1 EEVVPXGMHY 10
               EDMIQSGMHF 17
                                                                              Job time : 7.25 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:08:49; Search time 11 Seconds (without alignments) 96.134 Million cell updates/sec

1 eevvpxgmhys 11 AUDET-909-2 56 Perfect score: Sequence: Title:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

PIR 73:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ftsH proteinase ac	carbamoy1-phosphat	1	_	_	_	ρι	DNA binding protei	GMP synthetase, su	hypothetical prote	TSI8.1 protein - A	diphthine synthase	hypothetical prote	3-dehydroquinate s	probable DNA ligas	cell division prot	hypothetical prote	Sls1 protein precu	hypothetical prote	ATP-dependent DNA	hypothetical prote	polyamine transpor	conserved hypothet	probable amino aci	amino acid antipor	finger protein (cl	cytochrome-c3 hydr	coenzyme F420-quin	hypothetical prote
SUMMARIES	ID	A72207	F89892	A42452	AE2001	S69046	538143	D82618	T02590	H69194	T24111	G86430	G69117	C75538	B75478	T35025	E69086	C83903	S58132	T28717	AF3286	S54619	E83607	G82253	G71542	H81697	S65811	HQDVLB	$^{\circ}$	T08564
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æ	Query Match	66.1	66.1	64.3	64.3	4.	4.	ä	62.5	62.5	62.5	62.5	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	58.9	58.9	58.9	58.9	58.9	58.9	58.9	58.9	58.9
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DNA mismatch repai	macrophage-stimula	C14B9.8 protein -	L-shaped tail fibe	hypothetical 367K	tachykinin B precu	heme exporter prot	hypothetical prote	ribosomal protein	ribosomal protein	probable ThuA prot	hypothetical prote	cyclin D2 - rat	cyclin D2 - rat	cyclin D2 - mouse	cyclin D2 - human
A69663	JC5061	S44754	836851	T31308	A25905	D71640	S57810	E97120	T07215	C95881	T25737	JC4011	158372	A41984	A42822
N	-	~	~	7	~	~	~	7	N	~	~	~	7	~	7
627	716	1257	1396	3472	126	197	225	233	267	270	283	288	288	289	289
58.9	58.9	58.9	58.9	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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RESULT 1
```

fish proteinase activity modulator HflK - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Accession: A72207 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Nature 399, 323-329, 1999 A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ A,Reference number: A72200, MUID:99287316, PMID:10360571

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: MNA
A;Molecu

.; 0 Query Match 66.1%; Score 37; DB 2; Length 308; Best Local Similarity 75.0%; Pred. No. 10; Matches 6; Conservative 1; Mismatches 1; Indels

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Gaps

3 VVPXGMHY 10 ð

41 VVPSGIHY 48 셤

#### RESULT 2 F89892

carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: F89892

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001.
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A; Accession: F89892

A;Status: preliminary A;Molecule type: DNA

A;Residues: i-1057 <KUR>
A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
A;Experimental source: strain N315

C;Genetics:

A;Gene: pyrAB C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin c

Gaps

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A;Cross-references: EMBL:U43703; NID:g1244769; PIDN:AAB68221.1; PID:g1244776; MIPS:YPL135
C;Genetics:
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc R;anonymous, The Xylella fastidiosa dature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GN0012; A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrero, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohme A;Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-743 <VAN>
A; Cross-references: EMBL: Z28292; NID: 9486536; PIDN: CAA82146.1; PID: 9486537; MIPS: YKR067w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C,Species: Xylella fastidiosa
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Saccharomyces cerevisiae
C.baces 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C.pacession: S38143
R.yan Vliet-Reedijk, J.C.; Planta, R.J.
submitted to the Protein Sequence Database, March 1994
A.Reference number: S38130
A.Accession: S38143
                                                                                                                                                                                                                                                     A;Map position: 16L
C;Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
                                                                                                                                                                                                                                                                                                                                           Query Match 64.3%; Score 36; DB 2; Length 460; Best Local Similarity 62.5%; Pred. No. 25; Msmatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 743;
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Pred. No. 43;
1; Mismatches
                                                                                                                                                                                  A)Gene: SGD:UME1
A)Cross-references: SGD:S0006060; MIPS:YPL139c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: SGD:S0001775
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Best Local Similarity 75.v.
6; Conservative
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A; Reference number: S69040
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85 IVPLGLHY 92
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                       A;Accession: S69046
A;Molecule type: DNA
A;Residues: 1-460 <HAL>
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                              A42452

V. protein - tobacco yellow dwarf virus (strain Australia)

C. Species: tobacco yellow dwarf virus

C. Species: tobacco vellow dwarf virus

C. A2452

R. Morris: D.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

Virology 187, 633-642, 1992

A. Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow

A. Title: The nucleotide sequence number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Note: Nostco sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: Nostco sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AE2001 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. S. 2021 2001 A; Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUD:21595285; PMID:11759840 A; Status: preliminary A; A; Moleçule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
S69046
hypotherical protein YPL139c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Becies: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
C;Accession: S69046
C;Accession: S69046
C;Accession: J; Depended, A; Bussey, H; Fortin, N; Friesen, J.D.; Storms, R.K.; submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
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A;Experimental source: strain PCC 7120
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein alr1563 [imported] - Nostoc sp. (strain PCC 7120)
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                   66.1%; Score 37; DB 2; Length 1057; 60.0%; Pred. No. 39; 2; Indels tive 2; Mismatches 2; Indels
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Best Local Similarity 60.0%
                                                     Best Local Similarity 60.0
Matches 6; Conservative
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235 EMIVPAGLHF 244
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A; Residues: 1-102 <MOR>
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                   Query Match
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Gaps

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219 EEVVESGLHES 229
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A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Acdrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, F.R.; da Silvai, A.M.; Silvai Jr., W.A.; da Silvai, F.R.; da Silvai, A.M.; Silvai Jr., W.A.; da Silvai, F.R.; da Silvai, T.S.; Vettore, A.L.; Z. A;Contents: annotation
C;Genetics:
A;Gene: XF1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
C;Date: 05-Mar-1999 #sequence property in the common of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Residues: 1-311 cMTHA A,Residues: 1-311 cMTHA A,Cross-references: GB:AE000850; GB:AE000666; NID:g2621794; PIDN:AAB85215.1; PID:g262179 A,Experimental source: strain Delta H
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Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
Accession: H69194
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Best Local Similarity 55.0-
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Matches 6; Conservative
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Circlesion: G86430
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Attle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                                 A; Accession: T24111
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-425 «WIL»
A; Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSI8.1 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
Gaps
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Pred. No. 45;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 2; Length 425;
Pred. No. 37;
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C,Superfamily: hexose phosphate transport protein uhpT
                                                                                                                                                      submitted to the EMBL Data Library, October 1996 A; Reference number: 219842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 23/3; 56/3; 113/3; 257/2
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50.0%;
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Similarity 60.0%;
6; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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A;Molecule type: DNA
A;Residues: 1-510 <STO>
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                                                                                              C; Accession: T24111
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Gaps .

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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; J. Qiu, D.; Spadefora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. S.; Cubrch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 1135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession. G69117
A;Accession. A;Ac
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B75478
3-dehydroquinate synthase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
R;Accession: B75478
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein - Deinococcus radiodurans (etrain R1)
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C.Accession: C7558
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms.; Shith, H.O.; Vanter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Vonter, J.C.; Fraser, C.M.
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Recession: C75538
A;Recession: C75538
A;Residues: 1-279 <WHI>
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A;Experimental source: strain R1
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A,Gene: DR0271
A;Map position: 1
C,Superfamily: Deinococcus radiodurans hypothetical protein DR0271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 60.7%; Score 34; DB 2; Length 264; Best Local Similarity 62.5%; Pred. No. 35; Matches 5; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: MTH1874
C;Superfamily: Methanococcus jannaschii diphthine synthase
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A Status: preliminary
A Molecule type: DNA
A;Refidues: 1-350 <WHI>
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A;Cross-references: GB:AE001932, GB:AE000513; NID:g6458481; PIDN:AAF10353.1; PID:g6458486 A;Experimental source: strain R1 C;Genetics: C;Genetics: A;Gene: D7777 A;Map position: 1 C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C; Accession: T35025
R; Seeger, S:; Harris, D:; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A; Reference number: Z21565
A; Reference number: Z21565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL079355; PIDN:CAB45581.1; GSPDB:GN00070; SCOEDB:SC4C6.17c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                    60.7%; Score 34; DB 2; Length 350; 60.0%; Pred. No. 48; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.7%; Score 34; DB 2; Length 355; Best Local Similarity 71.4%; Pred. No. 49; Matches 5; Conservative 1; Mismatches 1; Indels
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A;Molecule type: DNA
A;Residues: 1-355 <SEE>
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Job time: 12 secs
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Best Local Similarity 60.0
Matches 6; Conservative
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Sequence 7, Appli
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Sequence 19, Appl
Sequence 2, Appli
                                                                   June 4, 2003, 13:09:19; Search time 9.75 Seconds (without alignments) 33.195 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-821-118-2
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US-09-134-001C-3950
US-08-134-001C-3950
US-08-134-001C-3950
US-08-134-001C-3950
US-08-199-955A-3
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Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:

Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 8, Appli Sequence 19, Appli Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 2, Appli Sequence 2, Appli		SEQUENCES RELATING TO STAPHYLOCOCCUS	Length 1037; 2; Indels 0; Gaps 0;		le No. 5821104th America, Inc.
US-08-246-361A-23 US-08-463-772-23 PCT-US93-05000-23 US-07-947-120-8 US-08-46-694-2 US-08-46-517-19 US-08-246-361A-19 US-08-246-361A-19 US-08-246-361A-19 US-08-246-37-20 US-08-246-37-20 US-08-463-772-20 US-08-463-772-20 US-08-463-772-20 US-08-947-492-8 PCT-US93-05000-2	ALIGNMENTS	09134001C  m et al  CID AND AMINO ACID  S2/99/134,001C  13  50/064,964  50/055,779	Score 39; DB 4; Pred. No. 16; 2; Mismatches		9 Aminopeptidas 821104disk of
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0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		:-001C-4794, Application US/, No. 6380370 INFORMATION: ANT: Lynn Doucette-Stam OF INVENTION: BPIDERMIISERENCE: GTC-007 TAPPLICATION NUMBER: US TELING DATE: 1997-11-08 APPLICATION NUMBER: US APPLICATION NUMB	69 63 rativ	HYS 11     HYS 209	Application US/088211 21104 RMATION: Holm, Kaj Andre Rasmussen, Grethe Halkier, Torben Lehmbeck, Jan NYENTION: Tripeptidy SEQUENCES: 23 ENCE ADDRESS: EN NO. 58211040 NO. 405 Lexington Avenue
57 57 57 57 57 57 57 57 57 57 57 57 57 5		1-001C-4794 No. 6380370 No. 6380370 N. INFORMATION: NINFORMATION: NUCLE OF INVENTION: NUCLE OF INVENTION: EPID EFERENCE: GTC-007 EFILING DATE: 1997-0 APPLICATION NUMBER: FILING DATE: 1997-0 APPLICATION NUMBER: FILING DATE: 1997-0 NO. 4794 H: 1037 H: 1037 H: 1037 H: 1037 H: 1037 H: 1137	h Similarity 7; Conserv	EEVVPXGMHYS:      :      KEVVSNGLHYS	19 Applicat 821104 "ORMATION: "I Rasmus "I Halkie "I Lehmbe INVENTION "SEQUENCE IDENCE ADD "EE: NO. 405 Lex NOW YORK
88888888888888888888888888888888888888		Sequence 4794 Sequence 4794, Application US/Patent No. 6380370 BRIERAL INFORMATION: APPLICANT: Lynn Doucette-Stam TITLE OF INVENTION: NUCLEIC A TITLE OF INVENTION: EPIDERNI FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US PRIOR PILING DATE: 1998-08 PRIOR FILING DATE: 1997-01-08 PRIOR FILING DATE: 1997-08-14 SEQ ID NO 4794 LENGTH: 1037 TYPE: PRT ORGANISM: Staphylococcus epi:	atc) cal	1 E) :	T SS H H H H H H H H H H H H H H H H H H
2 2 2 3 3 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5		RESULT 1 US-09-134-001C-4794 Sequence 4794, Ap. Patent No. 638037 GENERAL INFORMATI TITLE OF INVENTI TITLE OF INJENT TITLE OF TILING DATE RICH PRIOR APPLICATION PRIOR APPLICATION PRIOR PILING DATE PRIOR APPLICATION PRIOR PILING DATE TOWNERS OF SEQ ID NOWBER OF SEQ ID SEQ ID NO 4794 LENGTH: 1037 TYPE: PRT TYPE: PRT	Query M Best Lo Matches	Qy Db	RESULT 2 US-08-821-119 US-08-821-119 Patent No. GENERAL IN APPLICAN APPRES

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APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPPETIDE AMINOPEPTIDASE
TITLE OF INVENTION: ACTIVITY
CORRESPONDENCE: ACCOUNTY
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59898890 No. 5989889disk of No. 5989889th America, Inc.
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08821118
Patent No. 5989889
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                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.0°
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FRAGMENT TYPE: internal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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STATE:
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GENERAL INFORMATION:

APPLICAMY: LYND DOUGETEE-Stamm et al
APPLICAMY: LYND DOUGETEE-Stamm et al
APPLICAMY: LYND DOUGETEE-STAMM AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3950
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| Sequence 36, Application US/09724864 |
| Patent No. 6380362 |
| GENERAL INFORMATION: |
| APPLICANT: Watson, James D. |
| TITLE OF INVENTION: Polynucleotides, polypeptides expressed |
| TITLE OF INVENTION: By the polynucleotides and methods for their use. |
| FILE REFERENCE: 11000.1050U1 |
| CURRENT APPLICATION NUMBER: US/09/724,864 |
| CURRENT FILING DATE: 2000-11-28 |
| PRIOR FILING DATE: 1999-12-23 |
| NUMBER OF SEQ ID NOS: 72 |
| SOFTWARE: FERSTER OF SEQ ID NOS: 72 |
| SOFTWARE: RESTER OF Windows Version 4.0 |
| SOFTWARE: RESTER OF WINDOWS VE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 32; DB 4; Length 70; ilarity 62.5%; Pred. No. 19; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 600;
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3950, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                    60.7%;
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75...
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.43
Matches 5; Conservative
                                                                                                                         MOLECULE TYPE: protein
FRAGMENT TYPE: internal
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627 PGGLHYS 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VPKGWHYS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PXGMHYS 11
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US-09-134-001C-3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Fas
SEQ ID NO 36
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-724-864-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-724-864-36
                                                                                                                                                                                                            US-08-821-118-2
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Sequence 23, Application US/08580988A
Sequence 23, Application US/08580988A
Sequence 23, Application US/0858098A
Sequence 23, Application US/0858098A
Sequence 23, Application US/0858098A
SEQUENCE SEQUENCE
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 1.44 Mb floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/580,988A FLING DATE: January 3, 1996 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08879995A Patent No. 5985606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGI.
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                     ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EEVVPXGMHY 10
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36 MPKGFHYS 43
4 VPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: no
; FRAGMENT TYPE: i
; ORIGINAL SOURCE:
US-08-580-988A-23
                                                                                                                                                                                                                                                                                                       CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-879-995A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION
APPLICANT: Hallman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: *APPLICATION NUMBER: US/09/215,096
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastERD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0326 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                       COUNTR::

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"WANTER: IBM COMPATIBLE
THE TEM COMPATIBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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Best Local Similarity 66.7
Matches 6; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMH 9
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CA
                                                                                                                                                                                Palo Alto
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ö ö Gaps ö 57.1%; Score 32; DB 3; Length 152; 60.0%; Pred No. 44; 3; Indels Sequence 4, Application US/08460744

Patent No. 6107541

GABREAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600 Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and Its cDNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600 COUNTKI: ...
ZIN: 20005
ZIP: 20005
COMPUTER: ELORDY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OMPUTER: BY PC COMPATIBLE
OFFWARE: PATENTIN PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
TITING DATE: ...
435 60.0%; Pred. No. 44; tive 1; Mismatches 1; Mismatches ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFRENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600 not relevant INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 152 amino acids TYPE: amino acid STRANDEDNESS: not releva Best Local Similarity 60.0 Matches 6; Conservative Query Match
Best Local Similarity 60.0
Matches 6; Conservative 202-371-2540 TOPOLOGY: linear MOLECULE TYPE: peptide 1 BEVVPXGMHY 10 20 EEVFPLAMNY 29 1 EEVVPXGMHY 10 20 EEVFPLAMNY 29 Washington CITY: WASHINGTON STATE: DC COUNTRY: USA ŭ RESULT 11 US-07-667-711B-4 US-08-460-744-4 TELEFAX: CITY: STATE: ò g ò Gaps ; 0 57.1%; Score 32; DB 3; Length 126; 66.7%; Pred. No. 36; 7ative 1; Mismatches 2; Indels Sequence 4, Application US/08460694
Patent NO. 5558655
FATEL INFORMATION: Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC CUNNEY: USA

ZIP: 20005

ZIP: 20005

COUNTER: USA

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: O2-UM-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: MACCONARY, EVALUABES: 35,279
REFERENCE/POCKET NUMBER: 35,279
REFERENCE/POCKET NUMBER: 35,279
TELEPHONE: 202-371-260
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEMOTH: 125 amino acids
TVENEY: 202-371-254
INPORMATION CHARACTERISTICS:
LEMOTH: 125 amino acids NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNICE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION:
TELEPHONE: 415-855-0555 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE: INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 126 anino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear not relevant ATTORNEY/AGENT INFORMATION: TELEFAX: 415-845-4166 TOPOLOGY: linear MOLECULE TYPE: peptide 28 EQVVPGGGH 36 1 EEVVPXGMH 9 LIBRARY: GenBank CLONE: 163590 TYPE: amino acid STRANDEDNESS: no CLASSIFICATION: TOPOLOGY: line IMMEDIATE SOURCE:

US-09-215-096-3

RESULT 9 US-08-460-694-4

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FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCT-1992

APPLICATION NUMBER: US 07/888,178

FILING DATE: 26-MAY-1992

PRIOR APPLICATION NUMBER: US 07/701,514

FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:

REGISTATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MI-004C

TELECOMMUNICATION INFORMATION:

TELEFAX: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION CREATER: 16.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-246-361A-21
; Sequence 21, Application US/08246361A
; Patent No. 5998582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 amino acids
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Best Local Similarity 60.v
Best Local 6; Conservative
               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                    1 EEVVPXGMHY 10
                                                                                                                                                                                                          55 EEVFPLAMNY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                  US-08-193-977-7
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APPLICANT: WEBSTER, KEVIN R.
APPLICANT: WEBSTER, KEVIN R.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
NUMBER OF SEQUENCES: 3 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUMTRY: UNITED STATES OF AMERICA
ZIP: 94.901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
APPLICATION STATES OF AMERICA
CLASSIFICATION STATES
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Score 32; DB 3; Length 152; 60.0%; Pred. No. 44; tive 1; Mismatches 3; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
DPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMB: MCPHALL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMONICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TYPE: APPE: peptide
US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08193977 Patent No. 5625031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 EEVFPLAMNY 29
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                                                                                                                                                                                                                                                                                     Sequence 21, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
Query Match 57.1%; Score 32; DB 1; Length 173; Best Local Similarity 60.0%; Pred. No. 51; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%; Score 32; DB 2; Length 189; 60.0%; Pred. No. 56; 3; Indels tive 1; Mismatches 3; Indels
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Gaps
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
         APPLICANT: BEACH,
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.1%; Score 32; DB 2; Length 189; Best Local Similarity 60.0%; Pred. No. 56; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                STATE: MS
STATE: MS
COUNTRY: USA
ZIP: 02109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFCATION ATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALCHAW P. VINCENT
NAME: MALCHAW P. VINCENT
NAME: MALCHAW P. VINCENT
NAME: MALCHAW P. VINCENT
TELEFOUNDING (617) 227-7400
TELEFAX: (617) 227-5941
INPORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: LABORTERISTICS:
LENGTH: AND ACID
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
*OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
GENERAL INFORMATION:
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US-08-463-772-21
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Gaps
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Pred. No. 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       36,709
ER: MII-004C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 4, 2003, 13:14:59
Job time : 10.75 secs
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                   NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REPERBUCE/DOCKET NUMBER: MI:
TELECOMMUNICATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-08-463-772-21
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 EEVFPLAMNY 83
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Hepatitis C virus Hepatitis C virus
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                                                                                                                                                                                                                                                      (without alignments)
51.885 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT.
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT
                                                                                                                                                                                                             June 4, 2003, 13:04:09; Search time 28.25 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_101002:*
1: /SIDS2/gqqdata/geneseq/geneseqp-emb1/AA1980.
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80528
ABB80529
ABB80561
ABB80562
ABB80542
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ABB80542
ABB80542
ABB80521
                                                                                                                                          OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
                                 Copyright
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96.3
96.3
87.0
87.0
85.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
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-11 -11	epatitis C	atitis C	itis C	itis C	itis C	itis	citis C	itis C	itis C	itis C	itis C	itis C	itis	itis C	itis	citis C	itis C	citis C	itis	citis C	citis	epatitis C	atitis C v	atitis										
ABB80525 ABB80526	ABB80547	_					10	10	10	10	10	"	$\sim$ 1	3052	ABB80558	3056	3053	3053	8053	3053	3053	3054	3053	05	3054	3054	54	55	55	54	ABB80550	555	55	
23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	
11	11	11	11	11	11	11	11	11	11	11	11	H	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	
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11	13	14	15	16	17	18	19	20	21	55	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5	

#### ALIGNMENTS

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/note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
                                                                                                                                                                     note= "N-terminal acetyl"
                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                         note= "D-form residue"
                                                                                                                                                  Location/Qualifiers
                   ABB80524 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000US-220101P.
                                                           08-OCT-2002 (first entry)
                                                                                                                                                                                                                Misc-difference 9
                                                                                                                                                                                                                                                               WO200208251-A2
                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                               Synthetic.
                                       ABB80524;
RESULT 1
ABB80524
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activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                     Local Similarity 100.
nes 11; Conservative
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                                                                                                                                                                                                    1 EEVVPXGMDYS 11
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                                                                                                                                                                                 1 EEVVPXGMDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-361643/39.
                                                                                                                           11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
           virus protease
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                                                                                                                           Sequence
                                                                                                                                            Query Match
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                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                    'note= "N-terminal acetyl"
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                           Brunck TK;
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                                                                                                     Claim 17; Page 64; 69pp; English.
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        CORVAS INT INC.
                           Levy OE,
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                                             WPI; 2002-361643/39
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                                                                                    virus protease
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.3%; Score 52; DB 23; Length 11; 100.0%; Pred. No. 0.0015; ive 0; Mismatches 0; Indels
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Claim 17; Page 64; 69pp; English
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            invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
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                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
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                                                                                                                                  96.3%; Score 52; DB 23; Length 11; 100.0%; Pred. No. 0.0015; ive 0; Mismatches 0; Indels
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Best Local Similarity
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                                                Gaps
                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
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         ; DB 23; Lens
co. 0.0015; Indels
                      Length 11;
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                      96.3%; Score 52; 100.0%; Pred. No.
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                      Query Match
Best Local Similarity
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11 AA;
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Query Match

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    residue 7"
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Pred. No. 0.014;
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Pred. No. 0.0015;
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                                                                                                ABB80538 standard; peptide; 11 AA.
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        100.08;
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                  11; Conservative
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                                            1 EEVVPXGMDYS 11
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ABB80538
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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
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ABB80542 standard; peptide; 11 AA.
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virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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1 EEVVPXGQDYS 11

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Synthetic
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                                                                                               "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                               'note= "N-terminal acetyl"
                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                           'note= "D-form residue"
                                                                                                                                             /note= "D-form residue"
                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                         Brunck TK;
                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
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                                                                                                  /note=
                                                                                                                                                                                                                                                        CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
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                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                              virus protease
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                                                              Key
Modified-site
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                            virucide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HVV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treat associated with hepatitis C virus.
                                                                               "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
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                                           'note= "N-terminal acetyl"
                                                                                                                                                           "C-terminal amide"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 64; 69pp; English.
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90.9%;
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/note= '
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                                                                                             /note=
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus protease
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    Key
Modified-site
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21-JUL-2000; 2000US-220101P.
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                                                                                            virus protease
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                                    Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5
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                                                                                                                                                                                                                                                                                          Score 46; DB 23; Length 11;
Pred. No. 0.022;
0; Mismatches 1; Indels
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/note= "C-terminal amide"
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                                                                                                           Brunck TK;
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                                                                                                                                                                                Claim 17; Page 64; 69pp; English.
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90.9%;
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                                                     19-JUL-2001; 2001WO-US23169
                                                                       21-JUL-2000; 2000US-220101P
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                          Lim-wilby M, Levy OE,
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                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                               EEVVPXGMSYS
                                                                                                                            WPI; 2002-361643/39
                                                                                                                                                                                                                                                                         11 AA;
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                  WO200208251-A2
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                      Brunck TK;
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Best Local Similarity 90.9
Matches 10; Conservative
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(CORV-) CORVAS INT INC
                                                      Levy OE,
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08-OCT-2002
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                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide compound having hepatitis C virus protease inhibitory
try useful for treating disorders associated with hepatitis C
                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27
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                                                                                                                                                                                                                                                    Score 46; DB 23; Length 11;
Pred. No. 0.022;
                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                0; Mismatches
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/note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                            ABB80547 standard; peptide; 11 AA.
                                                                                Claim 17; Page 64; 69pp; English.
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                                                                                                                                                                                                                                                    85.2%;
90.9%;
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.>,,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                           1 EEVVPXGMDYS 11
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WPI; 2002-361643/39
                                                                                                                                                                                                                          11 AA;
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                                                       virus protease
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activity
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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    residue 7"
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 0.022;
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90.9%;
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
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                              Gaps
                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
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Score 46; DB 23; Length 11;
Pred. No. 0.022;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                              /note= "N-terminal acetyl"
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85.2%;
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Best Local Similarity 90.9
Matches 10; Conservative
                            10; Conservative
                                                                      1 EEVVPXGTDYS 11
                                                        1 EEVVPXGMDYS 11
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 Query Match
Best Local Similarity
Matches 10; Conserv
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0; Gaps

1 EEVVPXGSDYS 11

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1 EEVVPXGMDYS:11

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4, 2003, 13:11:13
Search completed: June
Job time : 28.25 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:07:09 ; Search time 22.5 Seconds (without alignments) 100.734 Million cell updates/sec

Run on:

Title: AUDET-909-3 Perfect score: 54 Sequence: 1 eevvpxgmdys 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL 21:*

1: SP_archea:*
2: SP_bacteria:*
3: SP_lungi:*
4: Sp_lungi:*
5: SP_inverebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organal:*
9: SP_organal:*
10: SP_organal:*
11: SP_roden:*
12: SP_virus:*
13: SP_virus:*
14: SP_virus:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	CANADAR OT SACCIDATION OF THE CONTRACTOR OF THE	030260 archaeoglob	O8rg86 fusobacteri			08w568 arabidonsis				043010 orvza sativ	088064 orvza sativ		OBXDAR Glostridium	052367 rhizobium t	O9xyk4 caenorhahdi	Q9a382 caulobacter
ID	012479	030260	Q8RG86	022081	022096	Q8W568	Q9C9T7	P93782	09SN30	043010	085064	090004	OBXPAB	052367	O9XVK4	Q9A382
DB	٣	17	16	10	10	10	10	10	10	10	10	'n	16	~	Ŋ	16
% Query Match Length DB	156	363	1063	341	348	452	460	1047	1083	1084	1100	219	253	298	425	433
% Query Match	74.1	70.4	70.4	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	64.8	64.8	64.8	64.8
Score	40	38	38	36	36	36	36	36	36	36	36	35	35	35	35	35
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5 3	Osop4e carcinus ma Q9u6a3 callinectes O17704 caenorhabdi		90	O9v9t6 drosophila		Q9vsy8 drosophila	Q9sbb8 oryza sativ	Q8r915 thermoanaer	Q8u7j0 agrobacteri			029451 archaeoglob		Q8tff4 trichoderma	Q8r8z2 thermoanaer		Q9jzp8 neisseria m				~	-
Q9YFI3 O52680 Q8XZL5	093548 09U6A3 017704	052673 052666	027146 098K29	09V9T6	Q8TBJ7	Q9VSY8	Q9SBB8	Q8R9L5	Q8U7J0	Q9YET8	029920	029451	Q98FX1	Q8TFF4	Q8R8Z2	Q9CIN1	Q9JZP8	Q9ZSY4	Q9FJK8	Q8W4J9	Q9ZSY3	Q9M5A1
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8.449 8.8.89		64.8 64.8	64.8		63.9	63.0	63.0	•	63.0	63.0	63.0	63.0		ω.	e.	ë.	63.0	63.0	ë.	63.0	63.0	63.0
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#### ALIGNMENTS

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Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395 (1994).

EMBL; Z74920; CAA99201.1; -.
SGD; S0005539; YOR013W.
SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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                                                                                                                                                                                                                                                                                                           74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 1.7;
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Pfam; PF00296; bac luciferase; 1.
Hypothetical protefn; Complete protecome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
earbamoyl-phosphate synthase large chain (EC 6.3.5.5).
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Archaeea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=VC-16 / DSM 4304 / ATCC 49558;
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EMBL; AE001109; AAB91255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein AF2411.
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Best Local Similarity 54...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ENIVPYGIDFS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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QBRG86
ID QBRG1
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DT 01-JI
DE Garbi
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030260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae,
eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=55188;
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                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 2586;
MEDLINE=21886394; PubMed=11889109;
MEDLINE=21886394; PubMed=11899109;
MEDLINE=21886394; PubMed=11899109;
MEDLINE=21886394; PubMed=1189109;
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Bhattacharyya A., Bartman A., Gardner W., Glechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. MIYAGAWA-WASE; TISSUE-JUICE SACS AND SEGMENT EPIDERMIS;
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Komatsu A., Takanokura Y., Omura M., Akihama T.; three sucrose
"Cloning and moleoular analysis of cDNA encoding three sucrose
phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                               70.4%; Score 38; DB 16; Length 1063; 60.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 341;
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                                                                                                                                                                                                                                                                                                             1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; Pred. No. 29; 2; Mismatches
           Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria, Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Gen. Genet. 252:346-351(1996).
                                                                                                                                                                                                                                                            J. Bacteriol. 184:2005-2018(2002).
EMBL; AE010554; AAL94625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Citrus unshiu (Satsuma orange).
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                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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195 EIVPNGLNYS 204
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es 6; Conserv
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                                               NCBI_TaxID=76856;
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49682 MW; A159955B21742C4A CRC64;

452 AA;

SEQUENCE

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SEQUENCE FROM N.A.

TISSUB-JUICE SACS AND SEGMENT EPIDERMIS;
Komateu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;

Nonferential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";

Plant Sci. 140:169-178(1999).

EMBL; AB006660; BAA22071.1;
                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Sapindales, Rutaceae, Citrus.
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96439842; PubMed=8842155;
Komatsu A., Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of cDNA encoding three sucrose
phosphate synthase isoforms from a citrus fruit (citrus unshiu
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF419606; AAL31931.; -.
InterPro; IPR003471; Prol_endopep_ser.
InterPro; IPR00379; Ser_estrs site.
PROSITE; PS00708; PRO_ENDOPEP_SER; UNKNOWN_1.
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348 348
348 AA, 38556 MW, EEIC21EBAGFF5C5E CRC64;
                                                                                                                           Created)
Last sequence update)
Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
At1g73750/F25F22_17.
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                                                                  348 AA
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TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
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                                                                  PRT;
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                                                                  PRELIMINARY;
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SEQUENCE
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RESULT 5
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SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA,

WHITE O., Alone O., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alone O., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alone O., Chao O., Chen H., Cheuk R.F., Chin C.W.,

Buehler B., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,

Dunn P., Etqu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A dill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khankin B.,

Kim C.J., Koo H.L., Kemenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,

Langin-Hooper J., Miranda M., Nguyen M., Nicarman W.C., Osborne B.I.,

Militscher J., Miranda M., Nguyen M., Nicarman W.C., Osborne B.I.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L., Tambunga G., Toriumi M.J., Town C.D.,

Wu Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

Wu D., Yu G., Fraser C.M., Vence J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702,
                                      Gaps
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0
 Length 452;
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Pred. No. 41;
0; Mismatches 3; Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 408:816-820(2000).

EMBL, AC012679; AAG52073.1; -
InterPro; IPR002471; Prol_endopep_ser.

InterPro; IPR000379; Ser_estrs site.

PROSITE; PSO0708; PRO_ENDOPEP_SER; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 460 AA; 50564 MM; E94B27B5C4B249EC CRC64;
                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 50.6 kDa protein.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
 DB 10;
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                                      0; Mismatches
                     40;
Score 36;
Pred. No.
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66.7%;
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70.0%;
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Best Local Similarity 70.000
                                      Conservative
                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                210 EEDVPSAMDY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 EEDVPSAMDY 227
                                                                           1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
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Query Match
Best Local Similarity
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                                      Matches
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Sugilation B., Sakakibara H., Sugiyama T.;
Sugilation B., Sakakibara H., Sugiyama T.;

"Differential Expression of Two Genes for Sucrose-Phosphate Synthase in Sugarcane: Molecular Cloning of the cDNAs and Comparative Analysis of Gene Expression. The EMBL/GenBank/DDBJ databases.

EMBL; AB001337; BAA19241.1; --

EMBL; AB001337; BAA19241.1; --

EMBL; AB001397; Glycos transf_1.

Pfam; PF00534; Glycos transf_1.

Pfam; PF00534; Glycos transf_1.

Glycosyltransferase; Transferase.
                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Saccharum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-MAY-2000 (TrEWBLrel. 20, Last sequence update)
01-MAY-2000 (TrEWBLrel. 20, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
F28M11.40 OR AT4G10120.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
11]
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Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 10; Length 1047;
Pred. No. 1e+02;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 36; DB 10; Length 1083; 66.7%; Pred. No. 1.1e+02; ive 2; Mismatches 1; Indels
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Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049487; CAB397641;
EMBL; AL16416; CAB397641;
InterPro; IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1.
Glycosyltransferase; Transferase.
SEQUENCE 1083 AA; 122688 MW; EFC126FCA2137BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
   Saccharum officinarum (Sugarcane)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.7
Nes 6; Conservative
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483 VIPPGMDFS 491
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                                                                                                                                         NCBI_TaxID=4547;
                                                                                                                                                                                                                                              TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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10 0958/30
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                                                                                                                                                                                                                               "Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Sasaki I., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 36; DB 10; Length 1084; 66.7%; Pred. No. 1.1e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                            SEQUENCE FROM N.A.
STRAINSCN. JAPONICA;
Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Pujimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 36; DB 10; Length 1100;
66.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone:P0678F11.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP003437; BAB86107.1; -.
SEQUENCE 1100 AA; 121170 MW; 084F4604BA389CAD CRC64;
                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
L-lactate dehydrogenase (EC 1.1.1.27) (LDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-UUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
          1084 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1100 AA
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                                    Created)
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P0678F11.14.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7 Matches 6; Conservative
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          PRELIMINARY;
                                  01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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469 VIPPGMDFS 477
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                                                                                                                                                     NCBI_TaxID=4530;
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          Q43010
Q43010;
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RESULT: 10

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RESULT 14
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                                                                                                                                                                           TISSUE-GILL;

Weihranch D., Towle D.W.;

"Na+/H+-exchanger and Na+/K+/2Cl--cotransporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis.";

Comp. Biochem. Physiol. 126:8158-8158(2000).

EMBL; AF301160; AAG39938.1; -.
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NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.8%; Score 35; DB 16; Length 253; 50.0%; Pred. No. 34; ive 3; Mismatches 2; Indels
                                                                                   Na+/K+/2Cl-cocransporter (Fragment).

Eriocheir sinensis (Chinese mitten crab).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Bucarida; Decapoda; Pleccyemata; Brachyura;

Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
                                                                                                                                                                                                                                                                                      64.8%; Score 35; DB 5; Length 219; 75.0%; Pred. No. 29; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
EMBL. AP003185; BAB79763.1.;
InterPro; IPR0000594; Thif domain.
Pfam; PF00899; Thif; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete Sci. Rev. 253 AA; 27714 WW; 8140F79D3E0D7486 CRC64;
                                                                                                                                                                                                                                                                   219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein CPE0057.
                                              219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local Similarity 50.07
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.
6, Conservative
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108 EEIIPDDVDY 117
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STRAIN=13 / TYPE A;
PubMed=11792842;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         219
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SEQUENCE
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             RESULT 12
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Rosenblueth M., Hynes M.F., Martinez-Romero E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: ZINC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                               Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group, Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.8%; Score 35; DB 2; Length 298; 50.0%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
EMBL, 781:109; CAB03241.1;
InterPro; IPR000719; Buk pkinase.
Pfam; PF00069; pkinase; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF036920; AAC04779.1; -.
HSSP; P07846; ISGG.
InterPro; IRR002285; ADH_zinc.
InterPro; IRR0022085; Adh_zn family.
InterPro; IRR002005; NAD_binding.
Pfam; PF00107; adh_zinc; 1.
Oxidoxeductase; Plasmid; 2.
NON TER 298 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.8
Best Local Similarity 50.0
Matches 5; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |::| | |:|
250 EIIPEGADFS 259
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                                                                                                                                                     Plasmid pRtrCFN299a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R10D12.10 protein.
R10D12.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                               Rhizobium tropici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                      NCBI_TaxID=398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XVK4;
                     052367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09XVK4
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·
0
                                                          0; Gaps
Query Match 64.8%; Score 35; DB 5; Length 425; Best Local Similarity 50.0%; Pred. No. 61; Matches 5; Conservative 3; Mismatches 2; Indels
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1 EEVVPXGMDY 10 |::|| |: | 335 EQIVPGGLQY 344 දු පු

Search completed: June 4, 2003, 13:13:26 Job time: 23.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:04:34; Search time 6.25 Seconds Run on:

(without alignments)
72.998 Million cell updates/sec

AUDET-909-3 Perfect score:

1 eevvpxgmdys 11 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Maximum Match 100% Post-processing: Minimum Match 0%

Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARIES

SUMMARIE SUMMARIE SUMMARIE SPS GRYSS SPS GRYSS SPS GRYSS SPS GRAPI FALL HUMAN PLAS CRAPI FALS CRAPI FALS CRAPI FALS CRAPI FALS CRAPI SPIAS CRAPI PLAS CRAPI PLAS CRAPI PLAS CRAPI PLAS CRAPI SYSP BORBU VS 39 WETJA BCD HALEL BCD HALEL BCD HALEL BCD HALEL BCD HALEL BCD HALEL BCD HALEL BCD THOMAN SUL SCHOOL SUL	SUMMARIES		Description .	FUSIN Q8rg86 fusobacteri	TYDVA P31619 tobacco yel			L 004933	_	Q9nr64	P20423	hordeun	P11970	P94283 borreli	Q58349	69v460		P08503	052250	09zeu7	060344	Q61851	P18460	074377	P27399	Q9kv29	P15822 homo sa	P19102	CA P2042	Q04667	ri Ci	SALTY P06190 salmonella	THEMA Q9wzr1 thermotoga	7 rattu	P30279 homo	# COCCCC
			DB	-	H	Н	Н	Н	Н			Н	Н		H	Н	Н	Н	ч	Н	Н	Н	Н	Н	Н	7	٦	Н	П	٦	٦	н	Н	Н	Н	
			Length	1058	102	1049	1068	1081	2747	748	154	155	168	999	276	283	394	421	421	423	787	801	908	877	982	1401	2717	472	97	175	231	231	3	æ	ω	
	,	* Ouery	Match	. 0	66.7	66.7	66.7	66.7	64.8	63.9	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1					59.3	59.3	59.3	59.3	59.3	
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PROSITE; PS00866; CPSASE_1; 2.

Q90459 brachydanio P50755 xenopus lae	P53782 xenopus lae	P55169 gallus gall P30281 homo sapien	P24385 homo sapien	P25322 mus musculu P39948 rattus norv	030640 methanosarc	Q91712 xenopus lae	• •
CGD1_BRARE CGD1_XENLA	CGD2_CHICK CGD2_XENLA	CGD1_CHICK CGD3_HUMAN	CGD1_HUMAN	CGD1_MOUSE CGD1_RAT	MTBA_METBA	ET2B_XENLA	HNFB_XENLA
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32	3 3	322	32	9 3	32	32	32
3.4 3.5	36 37	, 88 9	40	41 42	43	44	45

### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWAY: Arginine biosynthesis.
-i- PATHWAY: Pyrimidine biosynthesis; first step.
-i- PATHWAY: Pyrimidine biosynthesis; first step.
-i- SUBUNT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
-i- SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                      Aspatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattanaryya A., Bartman A., Gardner W., Grechkin G., Zhu L., Savalera O., Chu L., Kogan V., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCZ 2586.", J. Bacteriol. 184:205-2018(2002).

-! CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Disphate + L-glutamare + carbamoyl phosphate.
                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthese ammonia chain)
                                                                                                                                                                                                     Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE010554; AAL94655.1; ALT INIT.
InterPro; IRR005493; CPase_L.
InterPro; IRR005493; CPase_L.D.
InterPro; IRR005491; CPase_L.D.
InterPro; IRR005491; CPase_L.D.
InterPro; IRR005481; CPase_L.D.
InterPro; IRR005481; CPase_L.D.
Pfam; PF002786; CPSase_L.Chain; 2.
Pfam; PF02786; CPSase_L.D2; 2.
Pfam; PF02786; CPSase_L.D2; 2.
Pfam; PF02786; CPSase_L.D3; 1.
Pfam; PF02786; CPSase_L.D3; 1.
Pfam; PF02786; CPSase_L.D3; 1.
                                      STANDARD;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=ATCC 25586;
                                                                                                                                                                                                                                         NCBI_TaxID=76856;
                                                                                                                                                                                   CARB OR FN0422
                                        FUSNN
                                                       QBRGB6;
                     CARB_FUSNN
RESULT 1
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                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92188539; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";
                                                           OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                    ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
              Arginine biosyntnesis; ......ATP-binding; Manganese; Complete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
PROSITE; PS00867; CPSASE_2; 2. Arginine biosynthesis; Ligase; Repeat;
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                                                                                                                                                                                                                                                                           70.4%; Score 38; DB 1; Length 1058; 60.0%; Pred. No. 7.8; 1ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.7; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIE0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M81103; AAA47947.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                          Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                          929
1058
546
1058
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7 QVVPSGINYS 16
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                                                                                                                                                                                                                                             1058 AA;
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ID Y11K_TYDVA
AC P31619;
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REPEAT
NP_BIND
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREPORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.
-i- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last sequence encoration update)
15-DEC-1998 (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Indica-IR36; TISSUE=Leaf;
MEDLINE=96235138; PubMed=8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO01296; Glycos transf_1.
Pfan: PF00534; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
22 29 POLY-GLY.
PRT; 1049 AA.
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STANDARD;
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SPS ORYSA
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RESULT 3

audet-909-3.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Lamiales, Lamiales incertae, sedis, Torenieae,
                                                                                                                                                                                                                                                                                        -!- PATHWAY: Sucrose synthesis.
-!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
-!- DEVELOPMENTAL STAGE: GERMINATUG SEEDS OR MATURE LEAVES.
-!- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                          FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                           STRAIN=CV. PIONEER 3184; TISSUB=Leaf;
MEDINE=2233837; PubMed=1840536;
Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A.;
"Expression of a maize sucrose phosphate synthase in tomato alters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            SUCTOSE 6-Phosphate.
ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose
                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR001296, Glycos transf 1.
Pfam, PF00534, Glycos_transf_1; 1.
Transferase, Glycosyltransferase, Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1081 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLY
                                                                                                                                                   leaf carbohydrate partitioning.";
Plant Cell 3:1121-1130(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97451773; PubMed=9306694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate glucosyltransferase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M97550; AAA33513.1; -. PIR; JQ1329; JQ1329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craterostigma plantagineum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 VIPPGMDFS 443
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                                                                                                                                                                                                                                                                                                                                                ENZYME FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4153;
                                        NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craterostigma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MaizeDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          004933;
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SPS2_CRAPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- PATHWAY: Sucrose synthesis.
-i- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
-i- FUNDSPHORYLATED. HOMEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
"Analysis of cDNA clones encoding sucrose-phosphate synthase in
relation to sugar interconversions associated with dehydration in the
resurrection plant Craterostigma plantagineum Hochst.";
Plant Physiol. 115:113-121(1997).
-!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
(Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease FAF) (Deubiquitinating enzyme FAF) (Ret facets protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 1081; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           sucrose 6-phosphate.
-!- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYL
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
POLY-GLU.
POLY-ARG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 116:985-1000(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y11795; CAA72491.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 VIPPGMDFS 453
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STRAIN=cv. Ilpoom; TISSUE=Leaf;
Lee J.-S.;
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
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REPEAT
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REAL; L0495;

REAL; L0495;

REAL; L0495;

REROPS; C19.007;

REROPS; REPORTS; C19.007;

REAL; ROSITE; PS00973; UCH 2 1; 1.

DR PROSITE; PS00973; UCH 2 2; 1.

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Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVII.
                                                                          ubiquitin + a thiol.

ALTENANTIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: BYE DISKS AND OVARIES.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
NUCLEAR MIGRATION AND CELLULARIZATION IN BARLY EMBRYOGENESIS AND COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
                                                          CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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MEDLINE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.;
The SCA8 transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 1; Length 2747;
Pred. No. 91;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHL1 HUMAN STANDARD; PRT; 748 AA. 09NR64; 09NR65; 09P238; 09H4X4; 16-COT-2001 (Rel. 40, Created) 16-COT-2001 (Rel. 40, Last sequence update) 16-COT-2001 (Rel. 40, Last sequence update) 16-COT-2001 (Rel. 40, Last annotation update) KLHL1 OR KIAA1490.
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1394 EVIVPDGQDFS 1404
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Matches 6, Conservative
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                                                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF THE BRAIN CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
complete sequences of 100 new cDNA clones from brain which code
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C11C43D8282F9FF9 CRC64;
                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic.
-! TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
-!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.9%; Score 34.5; DB 1;
80.0%; Pred. No. 29;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIAS_ORYSA STANDARD; PRT; 154 AA.
AC PLAS_ORYSA STANDARD; PRT; 154 AA.
AC 01-PEB-1991 (Rel. 17, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last amnotation update)
DF 15-JUN-2002 (Rel. 41, Last amnotation update)
DF 15-JUN-2002 (Rel. 41, Last amnotation update)
DF 15-JUN-2002 (Rel. 41, Last amnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; smouze, .....
PROSITE; PS50097; BTB; 1.
Cytoskeleton, Actin-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF252293, AAF81719.1; -.
EMBL, AF252279, AAF81716.1; -.
EMBL, AB040923; BAA96014.1; ALT_INIT.
EMBL, AL353738; CAC16128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 605332; -.
'InterPro; IPR000210; BTB_POZ.
'InterPro; IPR0001798; Kelch.
Pfam; PF000651; BTB; 1.
Pfam; PF001344; Kelch; 6.
PRINTS; PR00501; KELCHREPEAT.
                                for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82680 MW;
                                                                                                 [3]
SEQUENCE OF 179-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC: 6352; KLHL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 EEVVP-GMDF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00225; BTB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Molecular cloning and characterization of plastocyanin precursor in
                                                                                                      Protein Seq. Data Anal. 2:385-389(1989).

-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: LOOSELY BOND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.

-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae;
Triticeae, Hordeum.
                                                   STRAIN=cv. Japonica;
MEDLINE=89386623; PubMed=2780537;
Mano H., Kamo M., Tsugita A., Aso K., Nozu Y.;
"The amino acid sequence of plastocyanin from rice (Oryza sativa,
subspecies japonica).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                     Prince, arroutise; copper_blue.
PRINTS; PRO0156; COPPERBLUE.
PROSTIE; PR00196; COPPER_BLUE; 1.
PROSTIE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide. 57 CHLORDFLACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                     Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E45725D25B5F400D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                      PLASTOCYANIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-UIN-2002 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.8;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 155 AA
                                                                                                                                                                                                                                                                                                                                                                                                            PLASTOCYANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               COPPER
                                                                                                                                                                                                                                                                                                HSSP, P00289, 2PCF.
InterPro, IPR000923, BlueCu 1.
InterPro, IPR001235, Copper_blue.
                                                                                                                                                                                                                                                                  EMBL, AF093636, AAC78108.1; -. PIR, S06105, S06105. PIR, JT0352, JT0352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15577 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Bomi;
Nielsen O.S., Gausing K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 EDAVPSGVDVS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                 57
154
154
139
142
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94
139 1
142 1
147 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                          SEQUENCE OF 58-154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLAS HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAS_HORVU
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                                                                                                                                   STRAIN=cv. NK 1558;
MEDINE=54039081; bubmed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                          promoter region.";

Eur. J. Biochem. 217:97-104(1993).

-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: LOCABLY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
"The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues."; FEBS Lett. 225:159-162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y00704; CAA68696.1; -.
EMBL; Z28347; CAA82201.1; -.
PIR; S00206, S00206.
InterPro; IPR000923; BlueCu 1.
InterPro; IPR001235; Copper_blue.
Pfam; PF00127; Copper_blue.
Prom; PF00127; Copper_blue.
Prom; PF00123; COPPERBLUE.
PROSTIE; PS001235; COPPER BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 155; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
T - N (IN CV. NK 1558).
W, DAA7EABESF6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Plastocyanin B, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASTOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST
                             expression in different tissues.";
Lett. 225:159-162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Populus nigra (Lombardy poplar).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Italica; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15709 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 EDAVPSGVDVS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMDYS 11
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155
155
140
148
120
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148 1
120 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transit peptide
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLAT POPNI
P11970;
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SEQUENCE
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RESULT 12
Y939_METJA
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0
                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                       Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
"Complete amino acid sequence of poplar plastocyanin b.";
FEBS Lett. 226.17-22(1987).
-i- FUNCTION: Participates in electron transfer between P700 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 35210 / B31,
Barbour A.G., Hinnebusch J.;
Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and
thioredoxin reductase gene of Borrelia burgdorferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        cytochrome b6-f complex in photosystem I.
-!- SUBSELLULAR LOCATION' LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
-!- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; PD001215; Copper Jlue; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family.
1 G9 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 168; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                      Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 AA; 16981 MW; F20DA6EA2038AEEA CRC64;
                                                                                                                                                                                                                                                                                POPLAR PLASTOCYANINS A AND B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetales, Spirochaetaceae, Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
  Haehnel W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; ZSVLGO,
PIR; SOD210; SOD210.
HSSP; POD299; IPLC.
INTERPRO; IPRO00923; BlueCu 1.
INTERPRO; IPRO01235; COpper_blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tRNA ligase beta chain) (PheRS)
Reichert J., Jenzelewski V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z50186; CAA90565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00127; copper-bind; PRINTS; PR00156; COPPERBLUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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112 EDAVPSGVDVS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMDYS 11
                                                                                   STRAIN=cv. Italica;
Dimitrov M.I., Egor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                               SEQUENCE OF 70-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHET OR BB0514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYFB BORBU P94283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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셤
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenhush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Ulterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03484; B5; i.
TIGRFAMs; TIGR00471; pheT_arch; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reitch C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
CHAIN FAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diphosphate + L-phenylalanyl-tRNA(Phe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.0%; Score 34; DB 1; Length 566; 85.7%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                              "Genomic seguence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001153; AAC66870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein MJ0939.
MJ0939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U82978; AAB41019.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               burgdorferi.";
Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 VPFGMDY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; BB0514; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y939 METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Gmith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Smrödy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pantoate--beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
(Pantoate activating enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diphosphate + (R) pantothenate.
-!- PATHWAY: Pantothenate biosynthesis; last step.
-!- SIMILARITY: BELONGS TO THE PANTOTHENATE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  61.1%; Score 33; DB 1; Length 276; 45.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004886; AAG08116.1; -.
InterPro; IPR003721; Pantoate_ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02569; Pantoate ligase; 1.
TIGRFAMs; TIGR00018; panC; 1.
                                                                                                                                                                                                                                                                                                                       EMBL; U67537; AAB98946.1; -.
                                                                                                         Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:: ||::|
141 EEIIENGMEHS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         TIGR; MJ0939; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PANC OR PA4730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANC PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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PANC_PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype O1;
STRAIN=El Tor N16961 / Serotype O1;
STRAIN=El Tor N16961 / Serotype O1;
MEDLITE=20406833; PubMed=10952301;
Heidelberg J.F. Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                 .
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Pfam; PF00175; NAD binding; 1.
Pfam; PF00175; NAD binding 6; 1.
PRINTS; PR00371; FPNCR.
PRINTS; PR00410; PHEMPORXLASE.
PROSITE; PS01033; GLOBIN; 1.
Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Flavohemogrotein (Hemoglobin-like protein) (Flavohemoglobin)
                                                DB 1; Length 283;
                                                                                 2; Indels
               283 AA; 30836 MW; C494949AB40E14E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON (HEME DISTAL LIGAND) (BY SIMILARITY).
Pantothenate biosynthesis; Ligase; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxygen transport; Transport; Complete proteome.
DOMAIN 1 136 GLOBIN.
                                                                                                                                                                                                                                 394 AA.
                                                                                 1; Mismatches
                                                61.1%; Score 33; DB 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001834; Cyt_B5_reductase.
InterPro; IPR001709; FPN cyt_redctse.
InterPro; IPR000971; Globin.
InterPro; IPR001433; Oxred FAD/NAD(P).
InterPro; IPR001221; Phe_hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE004358; AAF96096.1; -.
                                                              66.78;
                                                                               6; Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                96 ЕЕМҮРОСМО 104
                                                                                                               1 EEVVPXGMD 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXIDOREDUCTASES.
                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   HMP OR VCA0183.
Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIGE; VCA0183;
                                                                                                                                                                                                                                 VIBCH
                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae
                                                                                                                                                                                                                                 HMPA VIB
Q9KM<u>Y</u>3;
                                                                                                                                                                                                                HMPA_VIBCH
                                                                                 Matches
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audet-909-3.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
ACY1-COA dehydrogenase, medium-chain specific, mitochondrial precursor (RC 1.3.99.3) (MCAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBULT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-COA DEHYDROGENASES
OP DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 262:10104-10108(1987).
- FUNCTION: THIS ENZYME IS SPECIFIC FOR ACYL CHAIN LENGTHS OF 4 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRION.
ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G., Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.; "Molecular cloning and nucleotide sequence of CDNA encoding the entire precursor of rat liver medium chain acyl coenzyme A
                                          (BI SIMILMAKIII).
NADP (RIBOSE PART) (BY SIMILMRITY).
DDA3490FAE28823A CRC64;
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE ACYL-COA DEHYDROGENASE FAMILY.
                                                                                                                                                Score 33; DB 1; Length 394;
Pred. No. 30;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00441; Acyl-CoA_dh; 1.

Pfam; PF02770; Acyl-CoA_dh M; 1.

Pfam; PF02771; Acyl-CoA_dh M; 1.

PF027171; Acyl-CoA_dh M; 1.

PROSITE; PS00072; AcyL_COA_DH 1; 1.

PROSITE; PS00073; AcyL_COA_DH 2; 1.

Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism; Mitochondrion; Transit peptide.

*RAMOSTT 26 A21 ACYL-COA DEHYDROGENASE, MEDISCHAIN
IRON (HEME PROXIMAL LIGAND)
                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87280028; PubMed=3611054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001552; Acyl-CoA_dh.
                                                           268 273 N
394 AA; 44191 MW;
                                                                                                                                                   61.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J02791; AAA40670.1; -. PIR; A28436; DERTCM.
                                                                                                               Query Match
Best Local Similarity 66...,
Gonservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
82
                                                                                                                                                                                                                                                                                                                                           194 ÉVTPEGSDY 202
                                                                                                                                                                                                                                                                            2 EVVPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: FAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydrogenase.";
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver
                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACDM RAT
                                                       NP BIND
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METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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        FORMS A HYDROGEN-BOND WITH THE FLAVIN N(5) OF THE FAD COFACTOR (BY SIMILARITY). BASE (BY SIMILARITY).
                                                                                        Gaps
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0
                                                                Score 33; DB 1; Length 421;
Pred. No. 32;
                                                                                       3; Indels
                                           2CF076F8C919BDE8 CRC64;
                                                                                        2; Mismatches
SPECIFIC.
                                                                                                                                                                      Search completed: June 4, 2003, 13:11:46
Job time: 7.25 secs
                                            46555 MW;
                                                               61.1%;
50.0%;
                                                                                        5; Conservative
                                                                                                               1 EEVVPXGMDY 10
          193
                                                                                                                                   67
                                 401
                                                                                                                            ||::|
EEIIPVAPDY
                                             421 AA;
                                                                            Local Similarity
           193
                                 401
           ACT_SITE
                                 ACT SITE
                                             SEQUENCE
                                                                  Query Match
                                                                                        Matches
 8 5 5 5 5
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:08:49; Search time 11 Seconds Run on:

(without alignments) 96.134 Million cell updates/sec

AUDET-909-3 Perfect score:

1 eevvpxgmdys 11 Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1 prot	P _Z	V1 protein - tobac	sucrose-phosphate	sucrose-phosphate	unknown protein F2	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	hypothetical prote	peptidoglycan-bind	probable alkaline	hypothetical prote		fat facets (faf) s	plastocyanin b - L	plastocyanin precu	plastocyanin b pre	O6-methylguanine-D	6-0-methylguanine-	hypothetical prote		L-lactate dehydrog	ABC transporter AT	phenylalanine-tRNA	succinate dehydrog	disease resistance
SUMMARIES	ID	S54619	D69551	A42452	S72649	872650	G96764	JC4783	JQ1329	T09837	T04062	T04103	T24111	H87660	H72784	T20173	F69009	B49132	800210	S38255	S58208	D98182	AG3104	F72745	G69290	G69350	E86665	A70164	F81138	T48898
	DB	7	7	~	~	C)	7	~	Н	7	7	N	~	7	7	~	7	7	7	7	~	7	~	~	٦	~	7	7	~	~
	Length	156	363	102	341	348	460	1049	1068	1081	1083	1084	425	433	440	1150	1474	2747	66	155	168	290	290	296	357	366	299	266		0
de	Query	74.1	70.4	66.7	66.7	66.7	66.7	ė.	66.7	•		66.7	•	4.	٠	4.	4.	64.8	63.0				•	63.0				٠	٠	63.0
	Score	40	38	36	36	36	36	36	36	36	36	36	35	35	35	32	35	35	34	34	34	34	34	34	34	34	34	34	34	34
	Result No.	1	71	m	4	ហ	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

disease resistance	RND multidrug effl	hypothetical prote	hypothetical 367K	partial transposas	hypothetical prote	fibroblast growth	hypothetical prote	hypothetical prote	conserved hypothet	unknown protein [i	transposase ISC105	transposase ISC105	hypothetical prote	pantoate-beta-alan	transposase ISC105
T48899	F83335	T30830	T31308	A99427	A90471	S27021	E90335	S57810	A96001	A96546	F90298	C90307	C64417	G83055	E90487
~	~	7	7	N	0	7	0	N	7	7	N	7	0	N	7
906	1062	1062	3472	97	128	172	184	225	247	257	262	267	276	283	299
		_	0	Н	Н	Н	7	_	ч	_	_	_	Н	,	_
63.0	63.0	63.	63	61.	61.	61.	61.	61.	61.	61.	61.	61.1	61.	61.	61.
34 63.0	34 63.0									33 61.					

## ALIGNMENTS

hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3

C;Species: Saccharomyces cerevisiae C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002 C;Accession: S54619; S66879

R;de Haan, M.; Maarse, A.C.; Grivell, L.A. submitted to the EMBL Data Library, May 1995

A;Reference number: S54617 A;Accession: S54619

A; Molecule type: DNA A; Residues: 1-156 <DEH>

A;Cross-references: EMBL:X87331; NID:91041652; PIDN:CAA60762.1; PID:9829123 R;de Haan, M.; Grivell, L.A.; Maarse, A.C. submitted to the Protein Sequence Database, July 1996

A;Reference number: S66877 A;Accession: S66879

A;Molecule type: DNA A;Residues: 1-156 oLBW-A;Cross-references: EMBE: Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01: A;Experimental source: strain S288C

C; Genetics:

A,Cross-references: SGD:S0005539 A,Map position: 15R C,Superfamily: hypothetical protein YOR013w

ö Gaps ö 74.1%; Score 40; DB 2; Length 156; 77.8%; Pred. No. 1; tive 1; Mismatches 1; Indels Query Match
Best Local Similarity 77.8
Matches 7; Conservative

2 EVVPXGMDY 10 à

50 EVMPLGMDY 58 g

#### RESULT 2

conserved hypothetical protein AF2411 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

Cyaccesion: D6551

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Richemann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. A; Authores: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.A. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

;

Score 38; DB 2; Length 363; Pred. No. 6.8; 3; Mismatches 2; Indels

Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

-363 <KLE>

A; Molecule type: DNA

| : | | | : | 120 ENIVPYGIDFS 130

1 EEVVPXGMDYS 11

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Unknown protein F25P22.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: G96764

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L., Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alaunet 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; W., D.; Yu, G.; Fraser, C.M.; Wheter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; W. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719; PMID:11130712
                                                                                                        C;Accession: S72650
R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Rol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate synthas A;Reference number: S72648; MUID:96439842; PMID:8842155
A;Accession: S72650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-348 <KOM>
A;Cross-references: EMBL:AB006660; NID:92351059; PIDN:BAA22071.1; PID:92351060
A;Cross-references: EML:AB006660; Niyagawa-Wase
A;Experimental source: fruit, cv. Miyagawa-Wase
A;Nore: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C.Species: Citrus unshiu
C.Date: 24-0ct-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE005173; NID: 96692750; PIDN: AAF24856.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 2; Length 348; 66.7%; Pred. No. 17; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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70.0%; Pred. No. 23;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sucrose-phosphate synthase (EC 2.4.1.14) - rice C;Species: Oryza sativa (rice)
                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.vv,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Pathway: sucrose biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: G96764
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: SPS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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A42452

Y. protein - tobacco yellow dwarf virus (strain Australia)

C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
E;Anorias B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72649
R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha
A;Reference number: S72648; MUID:96439842; PMID:8842155
       A;Residues: 1-363 <KLE>
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g26506
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C, Superfamily: sucrose-phosphate synthase, sucrose-fucrose-phosphate synthase homology C, Keywords: glycosyltransferase; haxosyltransferase; sucrose biosynthesis
F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <8SPS>
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A;Residues: 1-341 <KOM>
A;Cross-references: EMBL:AB006319; NID:g2588891; PIDN:BAA23215.1; PID:g2588892
A;Experimental source: fruit, cv. Miyagawa-Wase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C;Genetics:
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872649
sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
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h Similarity 66.7%; Pred. No. 16; 6; Conservative 2; Mismatches 1. Tand-land

Local Similarity

Best Loc Matches

Query Match

A;Gene: SPS2 C;Function:

A;Accession: S72649 A;Status: nucleic acid sequence not shown

2; Mismatches

1:| ||:| 228 VIPPGMDFS 236

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RESULT 5

3 VVPXGMDYS 11

A; Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284

A;Accession: A42452 A;Molecule type: DNA A;Residues: 1-102 <MOR>

66.7%; Score 36; DB 2; Length 102; 60.0%; Pred. No. 4.2;

3; Mismatches

6; Conservative

Matches

Local Similarity

Query Match

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sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
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A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
A;Experimental source: subsp. Japonica
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A,Residues: 1-1083 <BEV>
A,Cross-references: EMBL:AL049487
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Matches 6; Conservative
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                                                                                                                                                                                                                A;Accession: JC4783
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1049 < vAL>
A;Residues: 1-1049 < vAL>
A;Cross-references: GB:U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A;Note: UDPglucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt C;Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and A;Gene: Sps1
    C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
C;Accession: JC4783
R;Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
Gene 170, 217-222, 1996
A;Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; 9 C.Function:
A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc A;Descriptions: biosynthesis sucrose biosynthesis sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
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C;Species: Craterostigma plantagineum
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09837
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Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
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nes 6, Conservative
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Plant Physiol. 115, 113-121, 1997
A,Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to sugary. A,Recession: T09837
A,Accession: T09837

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R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 1999
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
Plant Sci. 112, 207-217, 1995
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that
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C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Cybecies: Aeropyrum pernix
Amagica: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
Cybecoesion: H7284
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jamazaki, J.; Ki
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H7284
A;Status: Draiminary
A;Molecule type: DNA
A;Residues: 1-440 «KAW»
A;Residues: 1-440 «K
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Job time : 13 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.8%;
66.7%;
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Matches 6; Conservative
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120 EVLPWGVDY 128
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562 VLPVGIDYS 570
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Matches 6; Conserv
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                                                                                       RESULT 14
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, K.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzbay, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
                             A/Gene: Sps1
A/Map position: 1
A/Map position: 1
A/Introns: 120/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C/Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C/Keywords: glycosyltransferase; hexosyltransferase
C/Keywords: glycosyltransferase; hexosyltransferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
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A;Experimental source: clone R10D12
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A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
R;Percy, C
Submitted to the EMBL Data Library, October 1996
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Pred. No. 34;
2; Mismatches 3; Indels
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A;Accession: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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A;Gene: CESP:R10D12.10
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C; Genetics:
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A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 656
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A;Accession: T20173
A;Accession: T20173
A;Accession: T20173
A;Accession: proliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1150 «WIL>
A;Cross-references: EMBL:281486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
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Pred. No. 1e+02;
2; Mismatches 1; Indels
                                                                                           64.8%; Score 35; DB 2; Length 440; 66.7%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                         2; Mismatches
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A;Reference number: Z19808
A;Accession: T23857
A;Gene: APE0263
C;Superfamily: subtilisin; subtilisin homology
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                              June 4, 2003, 13:13:35; Search time 14.25 Seconds (without alignments) 79.694 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/Pub. Pub. Pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Description	Sequence 10, App.	Sequence	Sequence	Sequence	Sequence 9,	Sequence 27,	Sequence 5111, Ap	Sequence 4, Appli	Sequence 4, Appli	Sequence	Sequence 14,	Sequence 4881, Ap	Sequence 10697,	Sequence 526,	Sequence 526	Sequence	Sequence	Sequence	Sequence 420
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	00-10	8-00	00-4	00-11	6-00	08-27	242-5111	06-4	23-4	01-4	080-14	26-4881	US-09-815-242-10697	95A-526	97-526	92A-526	32A-526	89-526	90-420
	US-10-217-700-10	10-217-7	10-217-7	US-10-217-700-11	10-217-7	09-813-4	US-09-815-242-5111	10-027-8	US-10-034-623-4	10-027-8	US-09-948-080-14	JS-09-738-626-488;	-09-815-	JS-09-978-295A-526	JS-09-978-697-526	US-09-978-192A-526	8-666-60	09-978-1	US-10-174-590-420
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Query Match Length DB	1049	1068	1081	1083	1084	440	1062	3472	3472	3472	59	283	299	736	736	736	736	736	736
Query Match	66.7	66.7	66.7	66.7	66.7	64.8	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1
Score	36	36	36	36	36	35	34	34	34	34	33	33	33	33	33	33	33	33	33
Result No.	Н	7	m	4	2	9	7	æ	6	10	. 11	12	13	14	15	16	17	18	19

APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REPERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700

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| Publication NO. US20030070191A1
| GENERAL INFORMATION|
| APPLICANT: Holder A. Scott
| TILLE OF INVENTION| EXPRESSING FIBER PRODUCING PLANTS WITH INCREASED
| TILLE OF INVENTION| EXPRESSING FIBER PRODUCING PLANTS WITH INCREASED
| TILLE OF INVENTION| EXPRESSING OF SUCROSE PHOSPHATE SYNTHASE
| FILE REFERENCE: 201304/1000
| CURRENT APPLICATION NUMBER: US/10/217,700
| CURRENT FILING DATE: 1999-09-10
| MUMBER OF SEQ ID NOS: 14
| SOFTWARE FILING DATE: 1999-09-10
| NUMBER OF SEQ ID NOS: 14
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APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
TILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 1083
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CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
BARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ; ORGANISM: Craterostigma plantagineum US-10-217-700-4
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Sequence 11, Application US/10217700
Publication No. US20030070191A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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435 VIPPGMDFS 443
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                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Zea mays
US-10-217-700-8
                                                                                                                                           1068
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LENGTH: 1081
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APPLICANT: Delagrave, Simon
APPLICANT: Delagrave, Simon
APPLICANT: Delagrave, Simon
APPLICANT: Marra, Barry
TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial Lik,
TITLE OF INVENTION: Of Polynucleotides
FILE REFERENCE: HERO041
CURRENT APPLICATION NUMBER: US/09/813,408
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 85.
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; Bequence 9, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
APPLICANT: Holday, A. Scott
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REPERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/10/217,700
; CURRENT PILING DATE: 2002: 08/12
; EARLIER FILING DATE: 1999-09-10
; SARLIER FILING DATE: 1999-09-10
; SOFTWHARE: Patentin Ver. 2.0
; SEP ID NOS: 14
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Query Match 66.7%; Score 36; DB 9; Length 1083; Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches 1; Indels
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ORGANISM: Aeropyrum pernix
                                                                                                                                                      483 VIPPGMDFS 491
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                                                                                                        3 VVPXGMDYS 11
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
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LENGTH: 440
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ORGANISM: Cenarchaeum symbiosum
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45.5%;
2294 EDVIPRGISFS 2304
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Best Local Similarity 45.5
Matches 5; Conservative
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US-10-027-801-4
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Patent No. US2020160476A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REPERSENCE: DOORP.002A
CURRENT APPLICATION NUMBER: US.10/10/27,806
CURRENT FILING DATE: 2001-12-2/
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 09/408,020
NUMBER OF SEQ ID NOS: 123
SUSTINGER DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SUSTINGER DATE: 10005-123
SUSTINGER DATE: 10005-123
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45.5%; Pred. No. 9.1e+02;
iive 4; Mismatches 2; Indels
                                                                                                                                    APPLICANT: Wall, Daniel
APPLICANT: Transck, John D.
APPLICANT: Transck, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 0/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-21-6
PRIOR PRIOR PRIOR DATE: 2001-21-6
PRIOR PRIOR DATE: 2001-21-6
PRIOR PRIOR DATE: 2000-10-10-10-10-10-10-10-10-
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Pred. No. 2.4e+02;
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ORGANISM: Cenarchaeum symbiosum
                                                                                Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 85.7%;
Matches 6; Conservative
                        Haselbeck, Robert
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Best Local Similarity 45.5
Matches 5; Conservative
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                                                           Ohlsen, Kari
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US-10-027-806-4
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RESULT 9

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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 10; Length 59;
Pred. No. 15;
4; Mismatches 2; Indels
APPLICANT: HALKIER, TORDEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDITZ, PETER
APPLICANT: HANSEN, PETER RAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REPERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/09/948,080
CURRENT FILING DATE: 2001-09-06
PRIOR PILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASELSOF for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IXEDA, MASATO
APPLICANT: IXEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVORTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FPLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PRILING DATE: 1999-12-16
PRIOR PRILING DATE: 2000-04-07
PRIOR PLILNG DATE: 2000-04-07
PRIOR PLILNG DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 10697, Application US/09815242; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4881, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 EXHIPGGLEYS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VPXGMDYS 11
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US-09-815-242-10697
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LENGTH: 283
                                                                                                                                                                                                                                               SEQ ID NO 14
LENGTH: 59
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                        APPLICANT: Yanganou, Nobellian APPLICANT: Xu, Howard
TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILLING DATE: 2000-05-23
PRIOR PLILNG DATE: 2000-05-24
PRIOR FILLING DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,639
PRIOR PLILNG DATE: 2000-12-22
PRIOR PLILNG DATE: 2010-12-16
PRIOR PLING DATE: 2010-12-16
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Goddwark, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecalis
                                                                                     Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary E
                             Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:: | |::|
218 EQITPTGIEY 227
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APPLICANT: Haselbeck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-815-242-10697
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APPLICANT:
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PRIOR PILING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29 R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081071
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081195
R FILING DATE: 1998-04-08 R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082797
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082796
R FILING DATE: 1998-04-23
R APPLICATION NUMBER: 60/083336
R FILING DATE: 1998-04-27
R FILING DATE: 1998-04-27 R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083500
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083742
R FILING DATE: 1998-04-30
R APPLICATION NUMBER: 60/084366 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09
APPLICATION UNDRER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081819 FILING DATE: 1998-04-15 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081838 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21
APPLICATION UNMBER: 60/082704
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804 APPLICATION NUMBER: 60/081952 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/084414 FILING DATE: 1998-05-06 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084640 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084598 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/084637 PRIOR APPLICATION NUMBER: 60/08441 1998-04-08 FILING DATE: 1998-04-15 FILING DATE: 1998-04-22 FILING DATE: 1998-05-07

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PLING DATE: 1999-05-07
PRIOR PLING DATE: 1999-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
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PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08550
PRIOR PELING DATE: 1998-05-15
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 526, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
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Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Garo, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kljavin, Ivar J.
Kuo, Sophia S.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 EPVVVYGMDY 340
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US-09-978-697-526
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/978,697 CURRENT FILING DATE: 2001-10-16
                     CURRENT FILING DATE: 2001-10-16

REIOR APPLICATION NUMBER: 60/06220

PRIOR FILING DATE: 1997-10-13

PRIOR FILING DATE: 1997-10-13

PRIOR FILING DATE: 1997-10-13

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

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PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-21

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PRIOR PILING DATE: 1998-03-3-2

PRIOR PILING DATE: 1998-03-3-3

PRIOR PILING DATE: 1998-04-01

PRIOR PILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/08129
PRIOR PELING DATE: 1998-04-09
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PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-12
PRIOR PELING DATE: 1998-04-12
PRIOR PELING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/08136
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08136
PRIOR PELING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08156
PRIOR PELING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08156
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08159
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08159
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DAT

Search completed: June 4, 2003, 13:30:39 Job time: 15.25 secs

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Sequence 7, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 16, Appl
Sequence 14, Appl
Sequence 8, Appli
Sequence 6, Appli
Sequence 6, Appli
Patent No. 51771971
                                                                                                                                                June 4, 2003, 13:09:19; Search time 9.75 Seconds (without alignments) 33.195 Million cell updates/sec
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Sequence 6, A
Patent No. 517
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Sequence 4, A
Sequence 4, A
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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'cgn2_6/ptodata/1/jaa/5A_COMB.pep:*
'cgn2_6/ptodata/1/jaa/5A_COMB.pep:*
'cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
'cgn2_6/ptodata/1/jaa/6B_COMB.pep:*
'cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
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US-08-853-948B-5
US-09-697-367-24
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US-08-580-988A-23
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US-08-246-361A-21
US-08-246-361A-21
US-08-26-842B-20
US-08-46-517-22
US-08-46-517-22
US-08-46-517-22
US-08-46-517-22
US-08-46-361A-22
US-08-46-361A-22
US-08-246-361A-22
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US-08-070-165F-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                         OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                       Sequence:
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Sequence 21, Appl Sequence 6, Appli Sequence 6, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli		CITRUS AND DNA ENCODING	, Arg, Asn, Asp, , Lys, Met, Phe,	gth 341; Indels 0; Gaps 0;	CITRUS AND DNA ENCODING
28 32 59.3 240 3 US-08-926-842B-21 30 32 59.3 280 2 US-08-464-517-6 31 32 59.3 280 3 US-08-463-772-6 32 32 59.3 289 5 US-08-463-772-6 33 32 59.3 289 5 PCT-US93-05000-4 34 32 59.3 291 5 PCT-US93-05000-4 35 32 59.3 292 2 US-08-464-517-23 36 32 59.3 292 2 US-08-464-517-23 37 32 59.3 292 2 US-08-246-361A-23 38 32 59.3 292 2 US-08-246-361A-23 39 32 59.3 292 2 US-08-463-772-23 40 32 59.3 292 1 US-07-947-120-8 41 32 59.3 295 1 US-08-476-694-2 43 32 59.3 295 2 US-08-464-517-20 44 32 59.3 295 2 US-08-464-517-20 45 32 59.3 295 2 US-08-464-517-20 46 32 59.3 295 2 US-08-464-517-20 47 32 59.3 295 2 US-08-464-517-20 48 32 59.3 295 2 US-08-464-517-20 48 32 59.3 295 2 US-08-464-517-20	ALIGNMENTS	RESULT 1 US-08-853-948B-4  Sequence 4, Application US/08853948B  Patent No. 6210943  GENERAL INCERNATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: CURRENT APPLICATION NUMBER: US/08/853,948B  NUMBER OF SEQ ID NOS: 109  SEQ ID NO 4  LENGTH: 341  TYPE: PRATURE: TYPE: PRATURE	CTHER INFORMATION: Xaa at position 109 is one of Ala, OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, US-08-853-948B-4	Ouery Match Best Local Similarity 66.7%; Score 36; DB 4; Length Matches 6; Conservative 2; Mismatches 1; Ind Qy 3 VVPXGMDYS 11 Db 228 VIPPGMDFS 236	RESULT 2 US-08-853-948B-5 ; Sequence 5, Application US/08853948B ; Patent No. 6210434 ; GENERAL INFORMATION:    APPLICANT: AKTHAMA, TOYOTA ; TITLE OF INVENTION: THE SAME ; TITLE OF INVENTION: THE SAME ; TITLE OF INVENTION: THE SAME ; TITLE OF INVENTION: 1049-0235-0 ; CURRENT APPLICATION UNDER: US/08/853,948B ; UNDMBER OF SEQ ID NOS: 10 ; SEQ ID

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TYPE: Amino acid
STRANDEDNESS: Sin
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APPLICANT:
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APPLICANT:
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US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE;
APPLICANT: DEAN; VOELKER, TONI; GERVALS, MONICA
APPLICANT: DIAN; SUCKROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: SURPRATION METHOD AND CHNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CHARLES OF MODIFYING SPS EXPRESSION IN PLANT CELLS
TITLE OF INVENTION: CHARLES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: MIERRANA AND MUSERLIAN
                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 36; DB 4; Length 368; 66.7%; Pred. No. 16; tive 2; Mismatches 1; Indels
66.7%; Score 36; DB 4; Length 348; 66.7%; Pred. No. 15; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                 GENEKAL INFORMATION'S
APPLICANT: OTOZGO JI., EMIL M.
APPLICANT: OFOZGO JI., EMIL M.
APPLICANT: Gimi, Perry G.
APPLICANT: Weng, Zude
APPLICANT: TATCZYNSKİ, MİTCHELL
APPLICANT: TATCZYNSKİ, MİTCHELL
APPLICANT: TATCZYNSKİ, MİTCHELL
APPLICANTON: BRI166 US NA
CURRENT FILING DATE: 2000-10-26
CURRENT FILING DATE: 2000-10-26
CURRENT FILING DATE: 1998-MAY-07
PRIOR APPLICATION NUMBER: ECT/US99/09865
PRIOR APPLICATION UNMBER: PCT/US99/09865
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: MİCTOSOÉL OÉÉÍCE 97
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APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08429054A, Petent No. 5917126, GENERAL INFORMATION:
                                                                                                                                                                                                                                             Sequence 24, Application US/09697367
Patent No. 6323015
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600 THIRD AVENUE NEW YORK
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Query Match
Best Local Similarity 66.7%
Matches 6; Conservative
      Query Match
Best Local Similarity 66...
Feet Conservative 6, Conservative
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234 VIPPGMDFS 242
                                                                                                      3 VVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays
US-09-697-367-24
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US-08-429-054A-11
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SEQ ID NO 24
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US-09-697-367-24
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APERITION FELENSE #1.0, Version #1.30 SOCTAMES PARENTION Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777 FILING DATE: NOT YET ASSIGNED CLASSIFICATION: 800 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/175,471 FILING DATE: 27-DEC-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Law Offices of Barbara Rae-Venter STREET: 260 Sheridan Avenue, Suite 440 CTTY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE
TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Barbara Rae-Vent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.072.02US
TELECOMMUICATION INFORMATION:
TELEPHONE: (415)328-4400
TELEFAX: (415)328-4477
                                                                FILING DAIL. 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990
FILING DATE: 800
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-July-1991
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Compatible
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 7, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
                                                                                                                                                                                                            NAME: Charles A. Muserlian
REGISTRATION NUMBER: 19,683
REPERENCE/DOCKET NUMBER: 146.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEPK: (212) 661-8000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Assche, C.
Lando, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bruneau, J. M.
Voelker, T.
                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Unknown ; MOLECULE TYPE: Peptide US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single
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US-08-569-147-82
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APPLICANT: Shewmaker, C. K.

TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STRIET: California
                                                                                                                                                                                                   .;
0
                                                                                                                                                    66.7%; Score 36; DB 2; Length 1068; 66.7%; Pred. No. 53; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 3; Length 1068; 66.7%; Pred. No. 53; 1; Indels tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.110.02US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-CCT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-CCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP. 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barbara Rae-Venter. Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09051341
Patent No. 6124528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1068 amino acids
                                                                                                                                    Query Match
Best Local Similarity 66.74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     irPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-051-341-7
                                                                                          , MOLECULE TYPE: protein US-08-718-777-7
                                                                                                                                                                                                                                                         435 VIPPGMDFS 443
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                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-051-341-7
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CITY: Col
STATE: Oh
COUNTRY:
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Patent No. 5750365
GENERAL INFORMATION:
APPLICANT: Foulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: S2052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
CITY: Columbus
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                63.0%; Score 34; DB 4; Length 140; 75.0%; Pred. No. 13; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.1%; Score 33; DB 4; Length 59;
45.5%; Pred. No. 7.5;
cive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
FACENERAL INFORMATION:
FACENERAL INFORMATION:
FAPPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDITZ, BETER
APPLICANT: HAUDITZ, BETER
APPLICANT: HAUSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/08/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASISEQ for Windows Version 3.0
LENOTH: 59
            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yarko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:
TELEPRAX: (215) 568-3100
TELEPRAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecalis US-08-963-851-14
25-March-1996
                                                                                                                                                                                                                     LENGTH: 140 amino acids
TYPE: amino acids
TOPOLOGY: 1inear
MOLECULE TYPE: protein
US-08-569-147-82
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Best Local Similarity 45.5
Matches 5; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 WPTGFDY 129
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UG-08-885-418-8
; Sequence 8, Application US/08885418
; Patent No. 592528
; Patent INFORMATION:
APPLICANT: Chiu, Ing-Ming
; APPLICANT: Poulin, Matthew L
; TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
; STREET: $2052 Davis Medical Research Center, 480 West
; STREET: 9th Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                             61.1%; Score 33; DB 1; Length 378; 85.7%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8033
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION: TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acide
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                            : 378 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85./۱
المالية وفي Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) MOLECULE TYPE: protein US-08-885-418-8
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 PPGMDYS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PXGMDYS 11
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: Ohio
RY: USA
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                               Score 32; DB 6; Length 65;
Pred. No. 13;
                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423 REFERENCE/DOCKET NUMBER: D5721CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35,423
---- D5721CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                      US-08-580-988A-23
; Sequence 23, Application US/08580988A
; Patent No. 5856161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
                                                   59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 6; Conservative
                                                        Query Match 59.3
Best Local Similarity 45.5
Matches 5; Conservative
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                                                                                                                                           1 EEVVPXGMDYS 11
                                                                                                                                                                                     52 KEICPGGMGYT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houston
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US-08-460-694-4
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               5177197-51
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PATENT NO. 5177197

PATENT NO. 5177197

PATENT NO. 5177197

APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; MERNSTEDT, CHRISTER; HELLMAN, ULF, MIYAZONO, KOHEI; CLAESSON-WELSH, LENA; HELDIN, CARL-HENRIK

LITHLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990

SEQ ID NO:51:
                                                                 ESUL: 11-6
US-09-31-14
US-09-31-14
US-09-31-15
Sequence 6, Application US/09383630A
Setent No. 6265632
GENERAL INFORMATION:
APPLICANT: AVNOR YAYON Et al.
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
TITLE OF CHONDRODYSPLASIA
CHONDRODYSPLASIA
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted
to an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 801;
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85.7%; Pred. No. 1.5e+02;
trive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/383,630A
FILLING DATE: 26-Aug-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION UNMBER: «Unknown»
FILLING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Friedmam, Mark M.
REGISTRATION UNDRER: 33,883
REPERENCE/DOCKET NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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nes 6; Conservative
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139 PPGMDYS 145
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| Sequence 4, Application US/08460694
| Patent No. S858655
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| GREERI NO. S858655
| GREERI NEORANITON: PRADI Cyclin and its CDNA NUMBER OF SEQUENCES: STEARE CONTRESS: ADDRESSEE: STEARE ESSLER, GOLDSTEIN & FOX P.L.L.C.
CITY: Washington Now York Avenue, N.W., Suite 600
| STATE: 1100 New York Avenue, N.W., Suite 600
| STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | STATE: DOSS | ST
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Search completed: June 4, 2003, 13:14:59 Job time: 9.75 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:04:09; Search time 28.25 Seconds (without alignments) 51.885 Million cell updates/sec

5EQ 47 AUDET-909-4 55 1 (eevvpvgmsys 11) Title: Perfect score: Sequence:

ALL COMMON AR'S

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:* | SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1985.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* | SIDS2/gcgdata/geneseq-embl/AA1986.DAT:* | SIDS2/gcgdata/geneseqp-embl/AA1988.DAT:* | SIDS2/gcdgata/geneseqp-embl/AA1988.DAT:* S2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* | SIDS2/gogdata/geneseq/geneseqp-emb1/AA1990.DAT: | SIDS2/gogdata/geneseq/geneseqp-emb1/AA1991.DAT: | SIDS2/gogdata/geneseq/geneseqp-emb1/AA1992.DAT: | SIDS2/gogdata/geneseq/geneseqp-emb1/AA1993.DAT: | SIDS2/gogdata/geneseq/geneseqp-emb1/AA1994.DAT: | SIDS2/gogdata/geneseq/geneseqp-emb1/AA1994.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1996.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1997.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: 'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query re Match Length DB I	DB	ID	Description
	50	90.9	11	23	ABB80521	Hepatitis C virus
7	50	90.9	11	23	ABB80522	Hepatitis C virus
٣	50	90.9	11	23	ABB80525	O
4	20	90.9	11	23	ABB80526	U
2	20	90.9	11	23	ABB80559	Hepatitis C virus
9	20	90.9	11	23	ABB80563	Hepatitis C virus
7	20	90.9	11	23	ABB80564	Hepatitis C virus
ω	50	90.9	11	23	ABB80565	Hepatitis C virus
60	20	90.9	11	23	ABB80566	U
10	20	90.9	11	23	ABB80567	7)

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9	ABB80524	ABB80528	ABB80529	ABB80561	ABB80562	ABB80523		ABB80535	ABB80536	ABB80539	ABB80540	ABB80558	ABB80560	ABB80544	ABB80545	ABB80549	ABB80552	ABB80553	ABB80530	ABB80538	ABB80542	ABB80543	AAU76810	ABB80537	ABB80541	ABB80547	ABB80548	ABB80551	ABB80556	ABB80557		ABG05826	17	ABB80546
23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	50	23	23	23	23	23	23	23			22	
11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11			11			11		20	11		11		11	11	7	1022	1022	1022	11
٠	e.	<u>.</u>	ω,	۳.	83.6	•	81.8	81.8	81.8	81.8	81.8		81.8	80.0	80.0	80.0	80.0	80.0	76.4	74.5	74.5	74.5	74.5	72.7	72.7	72.7	72.7	72.7	72.7	72.7	172.2	72.7	72.7	70.9
		46	46	46	46	45	45	45	45	45	45	45	45	44	44	44	44	44	42	41	41	41	41	40	40	40	40	40	40	40	40	40	40	39
11	12	13.	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33		35	36	37	38	39	40	41	42	43	44	45

ABB80521 standard; peptide; 11 AA. 08-OCT-20g2 ABBB0524 RESULT 1 ABB80521

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1. (first entry)

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

Synthetic.

note= "N-terminal acetyl" Location/Qualifiers Key Modified-site

/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" Modified-site Modified-site

11 /note= "C-terminal amide"

WO200208251-A2

31-JAN-2002 

19-JUL-2001; 2001WO-US23169.

21-JUL-2000; 2000US-220101P.

(CORV-) CORVAS INT INC.

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Matches
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                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2
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0
                                                                                                                                                                                          90.9%; Score 50; DB 23; Length 11; 90.9%; Pred. No. 0.0033; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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         Brunck TK;
                                                                                                                                                                                                                                                                                            ABB80522 standard; peptide; 11 AA.
                                                                               Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001WO-US23169
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         Levy OE,
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                                                                                                                                                                                                                                               EEVVPXGMSYS
                          WPI; 2002-361643/39.
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                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                          11 AA;
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                                                              virus protease
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         Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7" .
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
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Claim 17; Page 64; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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Gaps

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Indels

Pred. No. 0.0033; 0; Mismatches

90.98;

Conservative

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Best Local Similarity
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pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Pred. No. 0.0033;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-terminal acetyl"
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                                                                    90.98;
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EEVVPXGMSYS 11
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                                                                                   Local Similarity
                                         11 AA;
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Length 11;

DB 23;

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
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1 EEVVPVGMSYS
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
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90.9%; Pred. No. 0.0033;
ive 0; Mismatches 1; Indels
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/note= "C-terminal amide"
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        /note= "Norleucyl carbonyl forming keto-amide linkage
   with residue 7"
                                                                                                                                                                                                                                                                                                                                    Gaps
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keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46
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Pred. No. 0.0033;
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/note= "C-terminal amide"
                                  /note= "C-terminal amide"
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                                                                                                                                         Brunck TK;
                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English
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ses 10; Conservative
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                                                                                                                        (CORV-) CORVAS INT INC
                                                                                                                                         Lim-wilby M, Levy OE,
                                                                                                                                                          WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                                                             virus protease
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Modified-site
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Matches
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invoide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
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Pred. No. 0.0033;
0; Mismatches 1;
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/note= "C-terminal amide"
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19-JUL-2001; 2001WO-US23169.
                                            21-JUL-2000; 2000US-220101P.
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Best Local Similarity 90.5.
Best Local 10; Conservative
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                                                                                                (CORV-) CORVAS INT INC
                                                                                                                                              Lim-wilby M, Levy OE,
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                                                                                                                                                                                                                                                                                                  virus protease
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                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                 Gaps
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
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Pred. No. 0.0033;
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/note= "C-terminal amide'
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                                                             Claim 17; Page 65; 69pp; English.
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Best Local Similarity
                                                                                                                                                                                                                  11 AA;
                                virus protease
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a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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                                                                                      Score 50; DB 23; Length 11; Pred. No. 0.0033; 0; Mismatches 1; Indels
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Pred. No. 0.02;
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81.8%;
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                                                                                        Query Match
Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                  1 EEVVPVGMSYS 11
                                                                                                                                                                             EEVVPXGMSYS 11
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Best Local Similarity
                                                            11 AA;
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmacceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                 /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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                 ABB80529 standard; peptide; 11 AA.
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81.8%; Pred. No. 0.02;
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Misc-difference

Modified-site

Modified-site

Synthetic

08-OCT-2002

ABB80528;

RESULT 13 ABB80528 Modified-site

WO200208251-A2

31-JAN-2002

virus protease

Sequence

RESULT 14

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Gaps

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08-OCT-2002 (first entry)

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                     /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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81.8%; Pred. No. 0.02;
cive 0; Mismatches 2; Indels
                                                                                                                                           /note= "N-terminal acetyl"
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                                                                                                               Location/Qualifiers
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Best_Local Similarity 81.8 Matches 9; Conservative

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1 EEVVPXGMDYS 11

4, 2003, 13:11:13

Search completed: June Job time : 28.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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June 4, 2003, 13:07:09; Search time 22.5 Seconds (without alignments) 100.734 Million cell updates/sec Run on:

1 eevvpvgmsys 11 AUDET-909-4 55 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_unclassified:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
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sp_bacteriap:*
sp_archeap:* SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:* sp mhc:* 111: 12: 13: 14: 15: 16:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Q9bha5 plasmodium	Q9bh83 plasmodium	Q971s2 sulfolobus	Q98bp5 rhizobium l		Q97de7 clostridium	Q8r8k6 thermoanaer	Q8ss39 encephalito	Q9v7c7 drosophila	Q12479 saccharomyc	032330 clostridium	Q9wvw3 mycobacteri	Q96mul homo sapien	Q98fx1 rhizobium 1	QBr126 mus musculu	Q8vd18 mus musculu
ΩI	<b>О</b> 9ВНА5	Q9BH83	097152	Q98BP5	Q8RE56	Q97DE7	Q8R8K6	Q8SS39	Q9V7C7	Q12479	032330	Q9WVW3	Q96MU1	Q98FX1	Q8R126	Q8VD18
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6 Q8UH45 6 Q9X104 Q9XCT2 Q9URYB 6 Q8RG86 Q9A208 Q43733 Q9A201 Q9710 Q8710 Q8710 Q8710 Q8710 Q8710 Q8710 Q1412 Q1412 Q1412 Q1412 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1612 Q1	0 0 0 0
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### ALIGNMENTS

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Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;

Plasmodium falciparum choline transporter (PfSCT1) gene.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AY007375; AAK14816.1; -.

EMBL; AY007375; AAG17947.1; -.

InterPro; IPR002123; Acyltransferase.

Pfam; PP01553; Acyltransferase.

SEQUENCE 583 AA; 66917 MW; 2B2BFAE38395E049 CRC64;
                                                                                                                          Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833,
                                                                                                                                                                                                                                                                                                                        72.7%; Score 40; DB 5; Length 583; 66.7%; Pred. No. 14; 0; Indels ative 3; Mismatches 0; Indels
                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                           583 AA.
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01-UUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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Probable DNA ligase.
                                                                                                              NCBI_TaxID=381;
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Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
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                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                         SEQUENCE FROM N.A.

Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;

"Plasmodium falciparum choline transporter (PfSCT1) gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               y Match 72.7%; Score 40; DB 5; Length 583; Local Similarity 66.7%; Pred. No. 14; ne 6; Conservative 3; Mismatches 0; Indels
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Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL, AP000985; BAB66348.1; -.
                                                                                                                                                                                                                                                       InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;
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Isomerase; Hypothetical protein; Complete proteome.
SEQUENCE 219 Aa; 24541 MW; A4E9A3F2C4006D90 CRC64;
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Last annotation update)
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Putative ribose 5-phosphate isomerase.
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(TrEMBLrel. 21, Last anno
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les 7; Conservative
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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227 IIPVGLSYS 235
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                      SCT1.
Plasmodium falciparum.
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Choline transporter
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Sulfolobus tokođaji
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01-OCT-2001
01-JUN-2002
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Matches
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"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

DNA Res. 7:331-338(2000).
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Bentl. AE01632, AAL59465.1; Complete proteome: Hypothetical protein. SEQUENCE 209 AA, 24056 MM; E471F6C4911506DA CRC64;
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                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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70.0%; Pred. No. 20;
tive 2; Mismatches 1
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InterPro; IPR00977; DNA_ligase.
Pfam, PF01068; DNA_ligase, 1.
PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_I.
PROSITE; PS50160; DNA_LIGASE_A3; 1.
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NCBI_TaxID=76856;
Rhizobium loti (Mesorhizobium loti)
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MEDLINE=21082930; PubMed=11214968;
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MEDLINE=21886394; PubMed=11889109;
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Best Local Similarity 70.ux
Best Local 7; Conservative
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Matches 7; Conservative
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144 LVPVGISYS 152
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SEQUENCE FROM N.A.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Predicted ATPases of the HSP70 class involved in cell division.
FTSA3 OR TTE1990.
                                                                                                                                                                                                        Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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45.5%; Pred. No. 57;
tive 4; Mismatches 2; Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 84 AA; 9313 MW; A8E15B62F24DA00B CRC64;
                                                                        01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein CAC3530.
                           84 AA.
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                           PRT;
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Best Local Similarity 45.55
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 70.0
Matches 7; Conservative
                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=1488;
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                         297DE7
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QBR8K6
Q97DE7
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RESULT 8 088839

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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Am K.H., Doyle C., Batter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.N.,
Ballew R.W., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 933;
                                                                                                                                                                                                                                                            Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypochetical protein.
SEQUENCE 933 AA; 106883 MW; CA400EE3A7AFF7CF CRC64;
                                                                                        01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ATP-dependent RNA helicase (SKI2 subfamily)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%; Score 37; DB 5; 63.6%; Pred. No. 97;
   933 AA.
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                                                                Created)
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   PRT;
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EMBL; AL590444; CAD25278.1; -.
                                                             (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                              ECU04 0910.
Encephalitozoon cuniculi.
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PRELIMINARY;
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43 EAVVPVGAAYT 53
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les 7; Conserv
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6035;
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                                                             01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

A Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lei Y., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Ra Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Parle D. Shen H.,

RA Palazzolo M., Siden-Kiamos I., Simpson M., Skrupski M.P., Smith T.,

She B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,

Shriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Williams S.M., Woodage T., Weinsteck G.M., Weissenbach J.,

Rhe Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rhe Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rhe Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rhe Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rhe Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rhe Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYC2 encodes a factor involved in mitochondrial import of yeast
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 5; Length 1305;
Pred. No. 1.4e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003810; AAF58131.1; -.
FlyBase; FBGN0034024; CG12961.
GROHENCE 1305 AA; 152870 MW; 8640B93F47B6EF3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=FY1679;
De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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Mol. Cell. Biol. 13:6442-6451(1993)
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54.5%;
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Best Local Similarity 54.5.
Local 6; Conservative
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STRAIN=FY1679;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q12479;
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Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
"Identification of a gene cluster involved in glycopeptidolipid
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Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium
MEDLINE=94169519; PubMed=7764548;
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-
"Mypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395(1994).
EMBL; Z74920; CAA99201.1; -.
EMBL; X87331; CAA60762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=98053837; PubMed=9393688;

Heath R.J., Goldfine H., Rock C.O.;

A gene (plsD) from Clostridium butyricum that functionally substitutes for the sn-glycerol-3-phosphate acyltransferase gene (plsB) of Escherichia coli.";
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                                                                                                                                                    Score 36; DB 3; Length 156;
Pred. No. 21;
2; Mismatches 1; Indels
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                                                                                                            SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           v.-νων.1998 (TrEMBLrel. 05, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Sn-glycerol-3-phosphate acyltransferase. PLSD.
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Interpro; IPR002123; Acyltransferase.
Pfan; PF01553; Acyltransferase; 1.
Acyltransferase; Transferase.
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156 EIIPIGMS 163
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50 EVMPLGMDY
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Rhizobium loti (Mesorhizobium loti).

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Eckstein T.M., Brennan P.J., Inamine J.M., Belisle J.T.;

Eckstein T.M., Brennan P.J., Inamine J.M., Belisle J.T.;

Eckstein T.M., Brennan P.J., Inamine J.M., Belisle J.T.;

Eckstein T.M., Brennan P.J., Inamine J.M., Blisle J.T.;

Experimental control of gene cluster encoding daunorubicin resistance in two strains of Mycobacterium avium serovar 2.";

Submitted (FBE-1399) to the EMBL/GenBank/DDBJ databases.

EMBL, AF143772; AAD4207.1;

EMBL, AF125999; AAD20362.1;

EMBL, AF125999; AAD20362.1;

Methyltransferase; Transferase.

SEQUENCE 273 AA; 30749 MW; 6543F9CIC5FIB761 CRC64;
biosynthesis and of a gene cluster encoding daunorubicin resistance in two strains of Mycobacterium avium serovar 2."_i Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31891 fis, clone NT2RP7003304, weakly similar to YceA protein
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO56453; BAB71188.1;
InterPro; IPRO01763; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conserv
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
        Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                        Mesorhizobium loti.";
DNA Res. 7:331-338 (2000).
DNA Res. 7:331-338 (2000).
InterPro; IPR002933; Peptidase M20.
Pfam, PR01546; Peptidase M20; I.
Hydrolase; Complete protecome.
SEQUENCE 387 AA; 41180 MW; 131BFF8B64306829 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54.5 kba protein (Fragment).
Mus musculus (Mouse).
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                                                                                    SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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                                                     NCBI_TaxID=381;
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OM protein - protein search, using sw model

Run on:

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1 eevvpvgmsys 11 AUDET-909-4 55 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	DNA segregation AT	hypothetical prote	hypothetical prote	adenylosuccinate s	hypothetical prote	71	DNA ligase (AB0425	hypothetical prote	glycerol-3-phospha	probable sulfate p	sulfate permease -	hypothetical 367K	50S ribosomal prot			zinc finger protei	hypothetical prote	DNA-binding protei	Vl protein - tobac	cell division inhi	transcription acti	D2 -		D2 -	D2 -	D1 -	D2 -	D2 -	eappea - In milano
Д	B97355	E97333	S54619	S48515	A82984	AH2679	F97461	A72273	A41672	T39116	T40413	T31308	E90544	E75619	C42053	S22293	T16459	A34203	A42452	H69491	A36893	JC4011	158372	A41984	A42822	S57922	S57925	4	862730
DB	7	7	~	Н	~	7	~	N	N	7	7	7	7	N	Н	~1	7	7	~	7	7	α	~	7	7	~	N	N	N
קט	1498	84	156	433	488	541	573	664	827	840	877	3472	116	227	286	670	919	2717	102	252	271	288	288	289	289	291	291	291	291
% Query Match	69.1			Š.	65.5	S	S	65.5	65.5	65.5	65.5	65.5	63.6	63.6	63.6	63.6	63.6	63.6	61.8	61.8	61.8	61.8	61.8	61.8	61.8			61.8	61.8
Score	38	37	36.	36	36	36	3,6	36	36	36	36	36	35	35	35	35	35	35	34	34	34	34	34	34	34	34	34	34	34
Result No.	1	7	٣	4	2	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps ;

Query Match
67.3%; Score 37; DB 2; Length 84;
Best Local Similarity 70.0%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 1; Indels

cyclin D3 - human cyclin D1 - human cyclin D1 - mouse	cyclin D1 - rat hypothetical prote hypothetical prote	hypothetical prote hypothetical prote phosphotransferase	hairy wing suppres hypothetical prote hypothetical prote	ribose 5-phosphate probable membrane probable 3-isoprop hypothetical prote
B42822 A38977 A56523	JC2342 C85432 D71278	T41621 D72253 S46953	S01909 T20173 S57810	F90249 AB0338 A64451 T34536
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31 31	1 E E E 1 E A T	3.86 7.8 8.6	9 6 4 4 9 0 0 1	44 44 44 45 57 57 57 57 57 57 57 57 57 57 57 57 57

## ALIGNMENTS

	RESULT 1
	D97335 DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported] - Clost C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence revision 14-Sep-2001 #text change 14-Sep-2001
	C; Accession: B97355 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Baly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
-11-11	beduction. 103, 4023-4030, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 4020, 402
	A;Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Gene: CAC3709
	Query Match 69.1%; Score 38; DB 2; Length 1498; Best Local Similarity 60.0%; Pred. No. 54; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
	1 EEVVPVGMSY   : :   :
	UD 12/6 BULLFMGMST 1285
•	RESULT 2 B9733 hypothetical protein CAC3530 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: E9733 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J; Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Reference number: DNA A;Residues: DNA A;Residues: 1-84 <kur>A;Ross-references: GB:AE001437; PIDN:AAK81456.1; PID:g15026624; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Genetics:</kur>

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A;Gene: SGD:ADE12; MIPS:YNL220w
A;Cross-references: SGD:S0005164; MIPS:YNL220w
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                                                                                                                                                               65.5%;
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Matches 6; Conservative
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les 6; Conservative
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A; Residues: 1-541 < KUR>
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                                                                                                                                                                  Query Match
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A;Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
A;Experimental source: strain S288C
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A;Residues: 1-433 <DUE>
A;Zross-references: EMBL:Z71496; NID:g1302236; PIDN:CAA96123.1; PID:g1302237; GSPDB:GN00
A;Experimental source: strain S288C
C;Genetics:
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A; Residues: 1-433 < SHA>
A; Residues: 1-433 < SHA>
A; Residues: 1-433 < SHA>
A; Residues: 1-433 < SHA>
A; Residues: 1-433 < SHA>
B; Ohanjan, T.; Daignan-Fornier, B.; Krauss, G.
Submitted to the EMBL Data Library, March 1995
A; Description: Adenylosuccinate synthetase from Saccharomyces cereviseae.
A; Reference number: S53085
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-433 < CHA>
A; Residues: 1-433 < CHA>
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A; Residues: 1-433 < CHA>
A; Residues: S53085
A; Residues: S62044
A; Residues: S62044
A; Reference number: S62944
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                                                                                                                                                                                                          hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Species: O8-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; S66879
R;de Haan, M.; Masrse, A.C.; Grivell, L.A.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123 R;de Haan, M.; Grivell, L.A.; Maarse, A.C. submitted to the Protein Sequence Database, July 1996
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C, Superfamily: hypothetical protein YOR013w
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                      1 EEVVPVGMSY 10
                                                   EEVINVGVSY 77
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50 EVMPLGMDY 58
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A; Residues: 1-156 < DEH>
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Best Local Similarity
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A; Molecule type: DNA
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Cjaccession: A82984
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brisadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogan. A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-488 <STO>
A;Cross-references: GB:AE004942; GB:AE004091; NID:g9951607; PIDN:AAG08679.1; GSPDB:GN001:
A;Experimental source: strain PA01
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. Rage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellis ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Aththors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-dependent DNA ligase Atu0840 [imported] - Agrobacterium tumefaciens (strain C58, Dupc
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ster, E.W.
Afritle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AH2679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PA5294 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 24-Aug-2001
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                                                                                                                                                        Length 433;
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                                                                                                                                                    Score 36; DB 1;
Pred. No. 35;
2; Mismatches
A,Map position: 14L
C,Superfamily: adenylosuccinate synthase
C;Keywords: ligase; purine nucleotide biosynthesis
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A; Title: Transcriptional regulation of p90 with sequence homology to Escherichia coli gl)
A; Reference number: A41672; MUID:92084678; PMID:1721057
A; Accession: A41672
A; Molecule : type: mRNA
A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Residues: 1-927 < skli>A; Res
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DDP
A,Residues: 1-840 < HINN-
A,Cross-references: EMBL:AL132779; PIDN:CABG0015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A,Experimental source: strain 972h-; cosmid c869
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A,Experimental source: strain 972h-; cosmid c3H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-877 <LYN>
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                                                                                                                                                                                                                                                                                                Score 36;
Pred. No. 7
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75.0%;
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Best Local Similarity 77...
77. Conservative
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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349 VIPVGISY 356
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A;Gene: SPDB:SPAC869.05c
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                                                                                                                                                                                                                                                                                         DNA ligase (AB042527) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Date: 30-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: F97461
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Reference number: A97359; PMID:11743194
A;Recession: F97461
A;Accession: F97461
A;Accession: F97461
A;Residues: 1-573 *KUR>
A;Cossion: F97461
A;Residues: 1-573 *KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86647.1; PID:g15155825; GSPDB:GN00169
C;Genetics:
A;Map position: circular chromosome
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A;Cross-references: GB:AE001783; GB:AE000512; NID:g4981832; PIDN:AAD36352.1; PID:g498183
A;Experimental source: strain MSB8
C;Genetics:
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72273
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Tille: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUD:99287316; PMID:10360571
A;Accession: A72273
A;Status: preliminary
A;Molecule type: DNA
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hypothetical protein TM1277 - Thermotoga maritima (strain MSB8)
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Best Local Similarity 60.0
Matches 6; Conservative
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474 EQLVPVGKAY 483
                                                                                                                       442 EQLVPVGKAY 451
                                                        1 EEVVPVGMSY 10
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completed: June 4, 2003, 13:14:16
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Best Local Similarity 54.5-
6. Conservative
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Matches 6; Conservative
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274 DQVVPVGLS 282
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Job time : 11 secs
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                       C;Species: Cenarchaeum symbiosum
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T31308
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
J. Bacteriol. 180, 5003-5009, 1998
A;Title: Genomic analysis reveals chromosomal variation in natural populations of the un A;Reference number: Z20994; MUID:98422450; PMID:9748430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50S ribosomal protein 120 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24 May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14

By5619

hypothetical protein DRB0013 - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Species: Deinococcus radiodurans

C;Date: 0.3-lec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C;Accession: E75619

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12657.1; PID:g6460953; TIGR:DRB0d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                              A;Residues: 1-3472 <SCH>
A;Cross-references: EMBL:AF083072; NID:g3599393; PID:g3599394; PIDN:AAC62699.1
C;Superfamily: Cenarchaeum symbiosum hypothetical 367K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
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Pred. No. 3.4e+02;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                             A;Accession: T31308
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
hypothetical 367K protein - Cenarchaeum symbiosum
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54.5%;
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2294 EDVIPRGISFS 2304
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Matches 6; Conservative
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A; Residues: 1-227 <WHI>
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C,Accession: C42053
R;Haefliger, J.A.; Bruzzone, R.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Paul, D.L.
Biol. Chem. 267, 2057-2064, 1992
A;Hitle: Four novel members of the connexin family of gap junction proteins. Molecular cl
A;Reference number: A42053; MUID:92112940; PMID:1370487
                          C;Genetics:
A;Gene: DRB0013
A;Map position: megaplasmid
A;Genome: plasmid
A;Note: plasmid MP1
C;Superfamily: Deinococcus radiodurans megaplasmid hypothetical protein DRB0013
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A;Note: sequence extracted from NCBI backbone (NCBIP:76095)
C;Superfamily: gap junction protein
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                                                                                                                                                                                                                                                                           63.6%; Score 35; DB 2; Length 227; 54.5%; Pred. No. 28; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Kewords: gap junction; phosphoprotein; transmembrane protein F;1-23/Domain: intracellular #status predicted <INT1> F;24-41/Domain: transmembrane #status predicted <INT1> F;24-77/Domain: extracellular #status predicted <EE1> F;78-97/Domain: transmembrane #status predicted <INT2>
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Pred. No. 36;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap junction protein Cx33 - rat
N;Alternate names: connexin 33
C;Species: Rattus norvegicus (Norway rat)
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A; Experimental source: strain R1
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:04:34; Search time 6.25 Seconds (without alignments) 72.998 Million cell updates/sec

AUDET-909-4 55

1 eevvpvgmsys 11 Perfect score: Sequence:

Scoring table: 'BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			psen	_	P97564 rattus norv				rattu	homo	P15822 homo	tobac		rattu	homo	P30280 mus musculu	brachyda	xenopus		xenopu	gallı	homo	homo	mus n		Q9y616 homo sapien			Q01606 klebsiella		esche	310 homo sap	P41367 sus scrofa
SUMMARIES	OI.	1A9		NOM2 PSEAE	PLSB_MOUSE	PLSB_RAT			RL20_MYCPU		PLSB_HUMAN	ZEP1 HUMAN	Y11K TYDVA	POBR_ACICA				CGD1_BRARE	CGD1_XENLA	CGD2 CHICK	CGD2 XENLA	CGD1 CHICK	CGD3 HUMAN	CGD1 HUMAN	CGD1_MOUSE	CGD1 RAT	OAT6_HUMAN	SUHW DROME	YC10 METJA					ACDM_PIG
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	P450211 haemophilus							067287 aquifex aeo	P23622 neurospora
AROA_VIBCH	CYOA_HAEIN	CAO1 HUMAN	CAO1_MOUSE	CAO1_RAT	OATP_RAT	SYTC YEAST	SCT1_YEAST	MUS2 AQUAE	CY14_NEUCR
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34	36.	37 38	39	40	41	42	43	44	45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a "Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: BELONGS TO THE FTSK/SPOIIIE FAMILX.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SETALISEATC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325, PubMed=11466286;
MEDLINE-21359325, PubMed=11466286;
Mobiling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                  Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP BIND 675 682 ATP (POTENTIAL).
SEQUENCE 1498 AA; 168968 MW; FF42037A335A9649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007866; AAK81629.1; -.
EMBL; X65276; CAA46379.1; ALT FRAME.
InterPro; IPR002543; FtsK SpoIIIE.
Pfam, PF01580; FtsK SpoIIIE; 2.
Pfam, PF01580; FtsK SpoIIIE; 2.
Hypothetical protein; ATP-binding; Complete proteome.
NP_BIND 675 682 ATP (POTENTIAL).
                                    (Rel. 28, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
                                                                                           Hypothetical protein CAC3709. CAC3709.
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STANDARD;
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Matches 6; Conserva
                                                                                                                                                                                                          NCBI_TaxID=1488;
                                        01-FEB-1994
                                                             16-OCT-2001
Y1A9 CLOAB
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                   Q043<u>5</u>1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93388587; PubMed=8376380;
Seidler R., Hobert O., Johannes L., Faulhammer H., Krauss G.;
Zeidler R., Hobert O., Johannes L., Faulhammer H., Krauss G.;
"Characterization of two novel single-stranded DNA-specific
autonomously replicating sequence-binding proteins from Saccharomyces
cerevisiae, one of which is adenylosuccinate synthetase.";
J. Biol. Chem. 268:20191-20197(1993).
-!-FUNCTION: PLAYS AN IMPERIANT ROLE IN THE DE NOVO PATHWAY OF PURINE
NUCLEOTIDE BIOSYNTHESIS.
-!-CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: AMP blosynthesis; first committed step.
                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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BY SIMILARITY.
BY SIMILARITY.
D - G (IN REF. 4).
W, FFEEB44F46349570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shabes A.V., Andreichuk Y.V., Holmes W.M., Domkin V.D.; Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohanjan T., Daignan-Fornier B., Krauss G.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                        432 AA
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InterPro; PR001114; ABUCC synthtase.
Pfan; PF00709; Adenylaucc_synt; 1.
ProDom; PD001188; ABUCC_synthtase; 1.
TGRPAMS; TGR00184; PUTA; 1.
PROSITE; PS00513; ADBNYLOSUCCIN SYN 2; 1
PROSITE; PS01266; ADENYLOSUCCIN_SYN_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE12 OR YNL220W OR N1290.
                                                                                                                                                                                                                     STANDARD;
                                1276 EQKIPMGMSY 1285
1 EEVVPVGMSY 10
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236
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236
432 AA;
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P80210:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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SERAITE-20437337; PhO1;
MEDLINE=20437337; Pubhed=10984043;
Stroat C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Brody D.L., Coulter L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody D.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                NOTE CONTROL (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Probable multidrug resistance protein norM 2 (Na(+)/drug antiporter)
(Multidrug-efflux transporter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMs; TIGR00797; matE; 1.
Transport; Antiport; Sodium transport; Transmembrane; Inner membrane;
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
-!- SIMILARITY: BELONGS TO THE MULTI ANTIMICROBIAL EXTRUSION (MATE)
FAMILY. NORM (TC 2.A.66.1.1) SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - FUNCTION: FUNCTIONS AS A NA(+)/DRUG ANTIPORTER (BY SIMILARITY)
                               ;
                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
65.5%; Score 36; DB 1; Length 432; 75.0%; Pred. No. 15;
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                             0; Indels
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                               2; Mismatches
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Pfam; PF01554; UPF0013; 2.
              Local Similarity 75.0
hes 6; Conservative
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:959-964 (2000)
                                                                                          346 IPVGISYS 353
                                                             4 VPVGMSYS 11
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                                                                                                                                                                                                                                                                                                                                     Pseudomonas
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Query Match
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"Transcriptional regulation of p90 with sequence homology to
Escherichia coli glycerol-3-phosphate acyltransferase.";
J. Biol. Chem. 266:22834-23839(1991).
-!- CATALYTIC ACTIVITY: Acyl-CoA + sn-glycerol 3-phosphate = CoA + 1-acyl-serol 3-phosphate.
-- CATALYTIC ACTIVITY: Acyl-CoA + sn-glycerol 3-phosphate = CoA + 1-acyl-serol 3-phosphate.
-- PATHMAX: FIRST STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS. IT MAY
ALSO FUNCTION IN THE REGULATION OF MEMBRANE BIOGENESIS.
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                           Gaps
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--- TISSUE SPECIFICITY: HIGHEST LEVELS IN LIVER, INTERMEDIATE LEVELS
IN MUSCLE AND KIDNEY, AND LOWEST LEVELS IN LUNG AND BRAIN.
--- SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
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MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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16-OCT-2001 (Rel. 40, Last annotation update)
Glycerol-3-phosphate acyltransferase, mitochondrial precursor (RC 2.3.1.15) (GPAI) (P90).
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InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
Transmembrane; Mitochondrion; Transit peptide.
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Pred. No. 2
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66.7%; Pred. No.
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286 MVPVGLSYA 294
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Q61586;
01-NOV-1997 (Rel 35,
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349 VIPVGISY 356
                                                                          3 VVPVGMSYS 11
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                                                                                                                                                                                                                T 4
MOUSE
                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TOPOLOGY.
STRAIN=Spraque-Dawley; TISSUE=Liver;
MEDLINE=20493538; PubMed=10924502;
Balija V.S., Chakraborty T.R., Nikonov A.V., Morimoto T., Haldar D.;
"Identification of two transmembrane regions and a cytosolic domain of rat mitochondrial glycerophosphare acyltransferase.";
Tat mitochondrial glycerophosphare acyltransferase.";
J. Biol. Chem. 275:31668-31673(2000).
-!- CATALYTIC ACTIVITY: Acyl-COA + sn-glycerol 3-phosphate = COA + 1-
                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acyl-sn-glycerol 3-phosphate.
--- PATHWAY: FIRST STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS. IT MAY ALSO FUNCTION IN THE REGULATION OF MEMBRANE BIOCENESIS.
---- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRIÓN (POTENTIAL).
GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.
MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhat B.G., Wang P., Kim J.-H., Black T.M., Lewin T.M., Fiedorek F.T. Jr., Coleman R.A.;

"Rat sn-glycerol-3-phosphate acyltransferase: molecular cloning and characterization of the CDNA and expressed protein.";

Biophys. Acta 1439:415-423(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
PLSB RAT STANDARD; PRT; 828 AA.
P97556; P97566; P97565; O35349;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Glycerol-3-phosphat acyltransferase, mitochondrial precursor (BC 2.3.1.15) (GPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002123; Acyltransferase.
Bfam; PF01553; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C -> F (IN REF. 2).

S -> P (IN REF. 2).

L -> V (IN REF. 2).

L -> V (IN REF. 2).

ILF -> NLL (IN REF. 2).

R -> M (IN REF. 2).

SAGGL -> LPEP (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAGGL -> LPEP (IN
Q -> H (IN REF. 2)
G -> A (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Mitochondrion; Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U36771; AAB39470.2; ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99376617; PubMed=10446428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ACTIVITY.
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                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
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Best Local Similarity
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RESULT 5

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REATAINS-279.

REATAINS-279.

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REATAINS-279.

REQUIRES J., Peat N., Hayles J., Basham D., Bowman S.,

REQUIRES W., Peat N., Hayles J., Basham D., Bowman S.,

RECORD R., Brown D., Chillingworth T., Churcher C.M.,

REA Grollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

REA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

REA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

REA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,

REA HOLroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA HOLroyd S., Moules M., Leather S., McDonald S., McLean J.,

RA HOLroyd S., Moules M., Pearson D., Quail M., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Sannders D., Odeil C.,

RA Retton J., Simmonia M., Squares R., Squares S., Stevens K.,

Retton J., Simmonia M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R Eger P., Zimmermann W., Wedler H., Rainhardt R., Purnelle B.,

R Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimmez J., Sanchez M., del Rey F., Benito J.,

R Gerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

R Shpakovski G.V., Ussery D., Barrell B.G., Murse P.;

R Harre 415: Blal-880 (2002)

R Harre 415: Blal-880 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
-!- SIMILARITY: CONTAINS 1 STAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                877 AA
                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR002645; STAS.,
InterPro; IPR001902; Sulfate_transp.
Pfam; PF00916; Sulfate_transp; 1.
Pfam; PF01740; STAS; 1.
TIGRPAMS; TIGR00815; sulP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL031261; CAA20298.1; -.
                        349 VIPVGISY 356
3 VVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
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                                                                                                                                                           SULH SCHPO
074377;
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PROSITE; PS01130; SLC26A; 1. PROSITE; PS50801; STAS; 1. Transport; Transmembrane.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: Arginine biosynthesis.
-i- PATHWAY: Pyrimidine biosynthesis; first step.
-i- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERTINGATION OF THE PROPRESS OF THE PROPRESS OF T., Tykidis A., MEDLINE-21886394; PubMed=11889109; Repatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardher W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586."; J. Bacteriol. 184:2005-2018(2002).
J. Bacteriol. 184:2005-2018(2002).
CATALYTIC CATALYTY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                       65.5%; Score 36; DB 1; Length 877; 77.8%; Pred. No. 31; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                          56995A8493371E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterium.
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INEEPPO; IPR005483, CRase_L.
INTEEPPO; IPR005499; CPase_L.
INTEEPPO; IPR005480; CPase_L_D3.
                                                                                                                                                                                                                          96373 MW;
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ID CARB FUSNN STANDARD;
AC Q8RGB6;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                        148 VVPOGMSYA 156
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133
1161
1221
222
222
3292
3294
4424
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461
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573
773
7A3,
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es 7; Conserv
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InterPro; IPR001081; Ribosomal_L20.
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TRANSMEM
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Nucleic Acids Res. 29:2145-2153 (2001).
Nucleic Acids Res. 29:2145-2153 (2001).
INCIENTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL SUBUNIT, IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS OF THAT SUBUNIT (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).

352 ATP (POTENTIAL).

284 MANGANESE I (BY SIMILARITY).

298 MANGANESE I AND 2 (BY SIMILARITY).

300 MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

420 MANGANESE 3 (BY SIMILARITY).

431 MANGANESE 3 (BY SIMILARITY).

432 MANGANESE 3 (BY SIMILARITY).

434 MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                               Pfam; PF02/142; MOCO. 1 PF187. PROUNTS: PROUNDS: PROUNDS: PROUNDS: PROSITE; PROUNDS: CPSASE_1; 2. PROSITE; PS00867; CPSASE_2; 2. Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome. CARBOXYPHOSPHATE SYNTHETIC DOMAIN. 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosowal protein L20.
Mycoplasma pulmonis.
Bacteria: Firmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 1058;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
InterPro; IPR005481; CPase L N.
InterPro; IPR004362; MGS like.
Pfam; PF00289; CPSase L Chain; 2.
Pfam; PF02786; CPSase L D2; 2.
Pfam; PF02787; CPSase L D3; 1.
Pfam; PF02142; MGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL445563; CAC13434.1; -. MypuList; MYPU_2610; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0°,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 EIVPNGLNYS 199
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929
1058
546
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210
352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2107;
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REPEAT
REPEAT
NP BIND
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RL20_MYCPU
ID RL20 M
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                          Score 35; DB 1; Length 116;
Pred. No. 6.1;
1; Mismatches 1; Indels
PFAM, PF00453; Ribosomal L20; I.
PRINTS, PR0062; RIBOSOMALL20.
PLODOM; PLO12389; RIBOSOMALL20.
TIGRFAMS; TIGR01032; rplT bact; 1.
PROSITE; PS00937; RIBOSOMAL L20; 1.
Ribosomal protein; RTNA-binding; Complete protecome.
SEQUENCE 116 AA; 13565 MW; C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL) . POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gap junction alpha-6 protein (Connexin 33) (Cx33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M76534; AAA40998.1; -.
PIR; C42053; C42053.
InterPro; IPR000500; Connexin.
Pfam; PF00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
PROSITE; PS00408; CONNEXINS 1; 1.
                                                                                                                                                                                                                               Query Match 63.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gap junction, Transmembrane.

DOMAIN 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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411
76
163
184
208
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                                                                                                                                                                                                                                                                                                                                                                                                  68 VRPLGMSYS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20456683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:273-281(2000)
--- CATALYTIC ACTIVITY: Acyl-CoA + sn-glycerol 3-phosphate = CoA + 1-acyl-can-glycerol 3-phosphate.
--- PATHWAY: FIRST STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS. IT MAY ALSO FUNCTION IN THE REGULATION OF MEMBRANE BIOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MINIO OCCASO, 1970

PinterPro; 1PR00123; Acyltransferase.

Pfam; PF01553; Acyltransferase; 1.

Phospholipid biosynthesis; Transferase; Acyltransferase;

Phospholipid biosynthesis; Transferase;

Transmembrane; Mitochondrion; Transit peptide.

Transit peptide.

Transit peptide.

Transit peptide.

Transit peptide.

Transit peptide.

Transit peptide.

Transit peptide.

Transit peptide.

Transit peptide.

MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).

471 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial outer membrane (By similarity).
SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                              ;
0
                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycerol-3-phosphate acyltransferase, mitochondrial precursor
(EC 2.3.1.15) (GPAT).
                                                     63.6%; Score 35; DB 1; Length 286; 66.7%; Pred. No. 15; 1.ve 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashwell R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
286 CYTOPLASMIC (POTENTIAL).
32860 MW; A585266ACA2ACCF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93836 MW; E5CD321A23D0B65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                 828 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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EMBL; AB046780; BAB13386.1; -.
MIM; 602395; -.
                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 167-828 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.6%;
                                                                        Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                     ::|||||:|
274 DQVVPVGLS 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471
                                                                                                                               1 EEVVPVGMS 9
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                 286 AA;
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575
594
828 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               GPAM OR KIAA1560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                 PLSB HUMAN
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                     Query Match
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 DOMAIN
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                                                                                                                                                                                                                            RESULT 10
PLSB HUMAN
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Best Local Similarity

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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EP) (Major histocompatibility complex binding protein 1) (MBP-1) (Regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Biochemistry 31:3907-3917(1992).

-!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEUKIN-2 RECEPTOR, AND INTERPERON-BETA GENES. IT MAY ACT
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Blochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: BY MITOGEN AND PHORBOL ESTER.

DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fan C.M., Maniatis T.; "A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92232684; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
  .
                                                                                                                                                                               2717 AA.
  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=90169514; PubMed=2106471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF 2087-2142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 2113-2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X51435; CAA35798.1; -. PIR, A34203; A34203. PDB; 3ZNF, 15-JAN-92. PDB; 4ZNF; 15-JAN-92. PDB; 1BBO; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-CELL ACTIVATION.
5; Conservative
                                                                                                                                                                                 STANDARD;
                                                                             349 IIPVGISY 356
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                       3 VVPVGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                 HIVEP1 OR ZNF40.
                                                                                                                                                                               ZEP1 HUMAN
P15822;
                                                                                                                                                                                                                                                                                                                                              PRDII-BF1)
                                                                                                                                                            ZEP1_HUMAN
  Matches
                                                                                                                                         RESULT 11
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audet-909-4.rsp

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EMBL; L05770; AAC37162.1; -. InterPro; IPR000285; HTH_IC1R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1993 (Rel. 27, Created)
           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                  STANDARD;
                                                                  :||| |::||
7 QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 EVVPVARSY 134
                                                      2 EVVPVGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPVGMSY 10
                                                                                                                                                                                                                                                                               STRAIN=BD413 / ADP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=471;
                                                                                                                                                                                                                                                                                                                                                                                                                 REGULATORS.
                                                                                                                                                                                                                                  Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding.
DNA_BIND
MUTAGEN
                                                                                                                                POBR ACICA
Q43992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGD2 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                            RESULT 13
POBR_ACICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
CGD2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

BEDLINES-2188538,

Morris B.-9.188538,

Morris B.-9.18.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component of
"The advant warf virus reveals features of geminiviruses
infecting monocotyledonus plants.";

Virology 187:642(1992).
                         InterPro; IPR000822; Znf C2H2.

Pfam; PF00096; zf-C2H2; 5.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00355; ZnF C2H2; 4.

PROSITE; PS00028; ZINC FINGER.

PROSITE; PS00129; ZINC FINGER.

PROSITE; PS00129; ZINC FINGER.

Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                         63.6%; Score 35; DB 1; Length 2717; 66.7%; Pred. No. 1.6e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                     POLY-SER.
C2HC-TYPE (POTENTIAL).
ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OTL-1993 (Rel. 27, Last annotation update)
Hypochetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 102 AA.
                                                                                                                       ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov.
Pfam; PP01708; Gemini mov; T.
Hypothetical protein:
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M81103; AAA47947.1; -.
TRANSFAC; T00497; -.
Genew; HGNC:4920; HIVEP1.
MIM; 194540; -.
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    2405 VVPAGLTYS 2413
                                                                                                                                                                                                                         2092
2092
2108
2109
2116
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2109
2139
2088
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                                                                                                                                                                   981
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                                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                           2087
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                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                   ZN FING
DOMAIN
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ZN_FING
STRAND
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Y11K TYDVA
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MUTĀGEN 61 61 R->H: IN ADP249; LOSS OF ACTIVITY.

SEQUENCE 271 AA; 30764 MW; 40B7DA8531389084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Acinetobacter calcoaceticus.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.8%; Score 34; DB 1; Length 271; 77.8%; Pred. No. 23;
61.8%; Score 34; DB 1; Length 102; 60.0%; Pred. No. 8.5; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                    15-JTU-1999 (Rel. 38, Created)
15-JTU-1999 (Rel. 38, Last sequence update)
16-CTT-2001 (Rel. 40, Last annotation update)
P-hydroxybenzoate hydroxylase transcriptional activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 AA.
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Best Local Similarity
 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILINE=59011623; Pubmed=7926809;
HOSOKawa Y., Onga T., Nakashima K.;
Hodokawa Y., Onga T., Nakashima K.;
Hoduction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by prolactin in rat Nb2 cells.";
Gene 147:249-522(1994).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START) TRANSITION.
                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERLELYHERONINE KINASE HOLORINZME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SELECTIVITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene. CONFLICT 68 68 E -> G (TN RRP 2)
                                                                                                                        MEDLINE=93275661; PubMed=8502486;
Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
"The Vin-1 gene, identified by provirus insertional mutagenesis, is
the cyclin D2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 68 E -> G (IN REF. 2).
104 104 C -> V (IN REF. 2).
232 232 T -> A (IN REF. 2).
288 AA, 32826 MW, 4B522BF4E9835FC1 CRC64;
            16-OCT-2001 (Rel. 40, Last annotation update)
GJ/S-specific cyclin D2 (Vin-1 proto-oncogene).
CGND2 OR VIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGD2_HUMAN STANDARD; PRT; 289 AA. P30279; Q13955; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-APR-2002 (Rel. 41, Last annotation update) G1/S-specific cyclin D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
01-OCT-1993 (Rel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L09752; AAA41010.1; -. EMBL; D16308; BAA03815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00134; cyclin; 1. --
Pfam; PF02984; cyclin C; 1.
SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                           Oncogene 8:1661-1666(1993).
                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                              SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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OCCUPATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic organization, chromosomal localization, and independent expression of human cyclin D genes."; Genomics 13:565-574(1992)
-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINFYHREONIDE KINASE HOLOBUNYER COWPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-i- SIMILARITY: BELONGS TO THE CYCLIN PAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

BEDILINE-3205384; PubMed=8455931; Pathers G.; Peters G.; Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.; Cyclins D1 and D2 are differentially expressed in human B-lymphoid
SEQUENCE FROM N.A.

BEDLINE-92347651; PubMed=1386336;
Xiong Y., Menningard J., Beach D., Ward D.C.;

Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92347850; PubMed=1386335;
Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyajima N.;
Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR004367; Cyclin.
PEam; PF00134; cyclin; 1.
SMAN; PF02984; cyclin; 1.
PROSITE; PS00292; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
CONFLICT CALL CYCLINS; 1.
CONFLICT 167 KL -> NV (IN REF. 5).
CONFLICT 224 Z24 T -> NY (IN REF. 5).
SEQUENCE 289 AA; 33067 MW; E4ESFEF476D76D90 CRC64;
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EMBL; X68452; CAA48493.1; --
EMBL; D13629; BAA020802.1; --
EMBL; M80083; AAA109588.1; --
EMBL; M880083; AAA51928.1; --
EMBL; M88081; AAA51928.1; --
EMBL; M88081; AAA51928.1; JOINED.
EMBL; M88081; AAA51928.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene 8:1049-1054(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-240 FROM N.A.
                                                                                                                                                 human D-type cyclins.";
Genomics 13:575-584(1992).
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MIM; 123833; -.
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PIR; S26580; S26580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         cell lines.";
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61.8%; Score 34; DB 1; Length 289; 60.0%; Pred. No. 25;

0; Gaps 2; Mismatches 2; Indels 6; Conservative Matches

0;

1 EEVVPVGMSY 10 ||| |: |:| 74 EEVFPLAMNY 83

ò qq Search completed: June 4, 2003, 13:11:47 Job time: 7.25 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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79.694 Million cell updates/sec
                                                                                                                                                                              June 4, 2003, 13:13:35 ; Search time 14.25 Seconds
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PUB. WBW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392085 seqs, 103240269 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1 eevvpvgmsys 11
                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                              Run on:
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Description	Sequence 4, Appli	Sequence 4, Appli	4	667	Sequence 2, Appli	Sequence 53, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 54, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 111, App	Sequence 66, Appl		Sequence 108, App	108,	184,		108,
ID	US-10-027-806-4	US-10-034-623-4	US-10-027-801-4	US-09-738-626-6675	US-09-935-290-2	US-09-778-927A-53	US-10-024-066-2	US-10-024-066-4	US-09-919-497-54	US-10-101-921-4	US-09-925-731-2	US-10-270-333-111	US-09-947-387-66	US-10-214-766-43	US-09-924-340-108	US-09-992-600A-108	US-09-746-783-184	US-10-000-489-108	US-10-000-986-108
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Score	36	36	36	35	35	34	34	34	34	34	34	34	33	33	33	33	33	33	33
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1061, Ap Sequence 1061, Ap Sequence 12270, A Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 175, Appl Sequence 1754, Appl Sequence 1754, Appl Sequence 11724, A Sequence 1250, Appl Sequence 1250, Appl	Sequence 236, App Sequence 1245, Ap Sequence 234, App
9 US-09-738-626-4919 9 US-10-280-403-2 10 US-09-907-479-2 10 US-09-917-30-1 10 US-09-913-304-4 10 US-09-913-304-4 10 US-09-913-304-4 10 US-09-815-242-12270 9 US-10-101-4644-73 9 US-10-111-76-4 10 US-09-815-242-10384 9 US-10-151-76-4 10 US-09-915-242-10597 10 US-09-915-242-10597 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-915-242-10597 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-915-242-1172-9 10 US-09-815-242-1172-9 10 US-09-815-242-1172-9 10 US-09-815-242-1172-9 10 US-09-815-242-1172-9 10 US-09-815-242-1172-9 10 US-09-815-242-1172-9 10 US-09-815-242-1173-9 10 US-09-815-242-1173-9	US-10-153-668-236 0 US-09-764-864-1245 US-10-153-668-234
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### ALIGNMENTS

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Sequence 4, Application US/10027806
| Patent No. US200201060476A1
| GENERAL INFORMATION: Schledy 10027806
| APPLICANT: Swanson, Ronald V. APPLICANT: Feldman, Robert A. APPLICANT: Schleper, Christa APPLICANT: Schleper, Christa APPLICANT: Schleper, Christa C. TILLE REFERENCE: DCORP.002A
| TITLE OF INVENTION: NUMBER: US/10/027,806
| CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
| PRIOR PILING DATE: EARLIER FILING DATE: 1999-09-29
| NUMBER OF SEQ ID NOS: 123
| SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION:
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
ITILE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REPERENCE: DCORP. 102/10/034,623
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Cenarchaeum symbiosum
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2294 EDVIPRGISFS 2304
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3472
TYPE: PRT
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US-10-034-623-4
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US-10-027-806-4
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Sequence 4, Application US/10027801

Sequence 4, Application US/10027801

Sequence 4, Application No. US2030054364A1

SEDERAL INFORMATION:

APPLICANT: Swanson, Ronald V.

APPLICANT: Swanson, Rohest A.

APPLICANT: Schleper, Christa

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/027,801

CURRENT FILING DATE: 2001-12-21

PRIOR PAPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020

SPRIOR FILING DATE: ERLIER FILING DATE: 1999-09-29

NUMBER OF SEACY ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 3472

TYPE: PRT

ORGANISM: Cenarchaeum symbiosum
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Pred. No. 5.8e+02;
4; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                           SEQ ID NO 4
LENGTH: 3472
TYPE: PRT
GORGANISM: Cenarchaeum symbiosum
US-10-034-623-4
                                                                                                                                                                                                                                                                          65.5%;
54.5%;
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54.5%;
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
6; Conservative
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-10-027-801-4
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Sequence 2, Application US/09935290

Sequence 2, Application US/09935290

Publication No. US20030044948A1

GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: S6919, A NOVEL HUMAN ACYLTRANSFERASE AND USES THEREOF
FILE REFERENCE: MNI-186

CURRENT APPLICATION NUMBER: US/09/935,290

CURRENT FILING DATE: 2001-08-21

PRIOR FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 828
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US-09-778-927A-53
; Sequence 53, Application US/09778927A
; Sequence 53, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; TITLE OF INVENTION: UNGER: US/09/778, 927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR PAPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR FILING DATE: 2000-02-09
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 53
LENGTH: 254
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6675
LENGTH: 332
                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6675
                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0 Matches 6; Conservative
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Matches 5; Conservative
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ORGANISM: Homo sapiens
PEATURE:
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118 VLPVGMAY 125
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ORGANISM: Homo sapiens
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APPLICANT: Field, Loren J.
APPLICANT: Field, Loren J.
APPLICANT: Pasumarthi, Kishoke Babu S.
APPLICANT: Pasumarthi, Kishoke Babu S.
TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: 60/139,942
PRIOR APPLICATION NUMBER: 60/139,942
PRIOR APPLICATION NUMBER: PCT/US00/16827
PRIOR APPLICATION NUMBER: PCT/US00/16827
PRIOR FILING DATE: 1999-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 289
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Patent No. US20020166134A1

GENERAL INFORMATION:

APPLICANT: Field, Loren J.

APPLICANT: Field, Loren J.

APPLICANT: Pasumarthi, Kishore Babu S.

TITLE OF INVENTION: CARDIOMYCCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

FILE REFERENCE: 7037-450

CURRENT APPLICATION NUMBER: 60/139,942

PRIOR PILING DATE: 2001-12-18

PRIOR PILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 289
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                                                                                                     61.8%; Score 34; DB 10; Length 254; 60.0%; Pred. No. 83;
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; NAME/KEY: misc_feature
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-57A-53
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60.0%;
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Best Local Similarity 60.07
                                                                                                                                                6; Conservative
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; ORGANISM: Homo sapiens
US-10-024-066-4
                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
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US-10-024-066-4
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  Gaps
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APPLICANT: Mutter, George L.
TITLE OF INVENTATION:
TITLE OF INVENTATION:
PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0810/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: 2000-07-31
SEQ ID NO 54
LENGTH: 289
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Publication No. US20030022199A1

GENERAL INFORMATION:

APPLICANT: Nozu, Jun.Tchi

APPLICANT: TSuji, Akta

APPLICANT: TSuji, Akta

TITLE OF INVENTION: TRANSPORTER GENES OATP-B, C, D, AND E

FILE REFERENCE: 06501-104US1

CURRENT APPLICATION NUMBER: 2002-06-28

PRIOR APPLICATION NUMBER: PCT/JP00/06416

PRIOR APPLICATION NUMBER: PCT/JP00/06416

PRIOR APPLICATION NUMBER: 1999-09-10

NUMBER: OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.8%; Score 34; DB 10; Length 289; 60.0%; Pred. No. 95; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.8%; Score 34; DB 9; Length 691; Best Local Similarity 62.5%; Pred. No. 2.4e+02; Matches 5; Conservative 3; Mismatches 0; Indels
  2; Indels
  2; Mismatches
                                                                                                                                                                                       Sequence 54, Application US/09919497
Patent No. US20020106662A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09925731; Patent No. US20020090622A1
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Matches 6; Conservative
  6; Conservative
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                                         1 EEVVPVGMSY 10
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                                                                            74 EEVFPLAMNY 83
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US-10-101-921-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-919-497-54
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188 IVPLGLSY 195
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US-09-919-497-54
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US-09-925-731-2
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US-10-101-921-4
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    Matches
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US-09-924-340-108
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US-10-214-766-43
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Publication No. US20030092124A1
GENERAL INFORMATION:
APPLICANT: Cravchik, Anibal
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING GPCR. PROTEINS, AND USES
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        61.8%; Score 34; DB 10; Length 691;
62.5%; Pred. No. 2.4e+02;
tive 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILE REPERENCE: CLOOO733COM
CURRENT APPLICATION NUMBER: U5/10/270,333
CURRENT FILING DATE: 2002-10-15
PRIOR PELICATION NUMBER: 60/156,677
PRIOR PELING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
              APPLICANT: ADEOKON, ANTHONI MONISOLA
APPLICANT: AMBROSE, HELEN JEAN
APPLICANT: CRESSWELL, CARL JOHN
TITLE OF INVENTION: CHEMICAL COMPOUNDS
FILE REFERENCE: DJ8/009901/0282795
CURRENT APPLICATION NUMBER: US/09/925,731
CURRENT APPLICATION NUMBER: 60/226,909
PRIOR PILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 12.
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; Sequence 66, Application US/09947387
; Patent No. US20020150885A1
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APPLICANT: Weber, Eckard
APPLICANT: Cal, Sul Xiong
. APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62...
5, Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||:|:
188 IVPLGLSY 195
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 691
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LENGTH: 774
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TITLE OF INVENTION: No. US20020150885Alel Fluorogenic or Fluorescent Reporter Molecule
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REPERENCE: 1735.029005
CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT APPLICATION NUMBER: US 60/061,582
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1999-10-10
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver: 2.0
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TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
FILE REFERENCE: CA1138
CURRENT APPLICATION NUMBER: US/10/214,766
CURRENT APPLICATION NUMBER: US 60/311,734
PRIOR APPLICATION NUMBER: US 60/311,734
PRIOR PLILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 43
LENGTH: 426
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.052.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT PILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.0%; Score 33; DB 10; Length 10; Best Local Similarity 50.0%; Pred. No. 3.9; Matches 5; Conservative 3; Mismatches 2; Indels
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Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 43, Application US/10214766; Publication No. US20030084473A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 EFVIPAGOSY 232
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Page 5

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:09:19; Search time 9.75 Seconds (without alignments) 33.195 Million cell updates/sec

AUDET-909-4 55

1 eevvpvgmsys 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

262574 segs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

262574

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* ........

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

	Description	Sequence 236, App		236,	23, #	4,	4	4	7	21,	21,	21,	Sequence 21, Appl	22,	22,	22,	22,	9	9	Sequence 4, Appli	4,	ý	23,	9	23,	23	23	Sequence 8, Appli
SUMMARIES	ΙD	_	US-08-871-355A-236	US-09-201-945-236	US-08-580-988A-23	-08-4	-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	46	US-08-463-772-21	PCT-US93-05000-21	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22	US-08-464-517-6	US-08-463-772-6	US-08-246-361A-4	PCT-US93-05000-4		US-08-464-517-23	US-08-246-361A-6	US-08-246-361A-23	US-08-463-772-23	PCT-US93-05000-23	US-07-947-120-8
	DB	7		-	0			m	• •	•											-						Ŋ	
	Query Match Length	45	45	45	102	152	152	152	173	189	189	189	189	236	236	236	236	280	280	289	289	291	292	292	292	292	292	295
ф	Query	63.6	63.6	63.6	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8			61.8			61.8	ä	ä	61.8	Η.	ä	61.8	ä	ä	61.8
	Score	35	35	35		34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
	Result No.	н	7	3	4	ស	9	7	හ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		26	. 27

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0; Gaps

Query Match 63.6%; Score 35; DB 2; Length 45; Best Local Similarity 60.0%; Pred. No. 3.6; Matches 6; Conservative 2; Mismatches 2; Indels

Sequence 8, Appli Sequence 2, Appli	19,	Sequence 20, Appl Sequence 19, Appl	Sequence 20, Appl	20	Sequence 2, Appli	7	ω,	Sequence 2, Appli	Sequence 19, Appl	Sequence 20, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 8, Appli
US-08-472-893A-8 US-08-460-694-2	US-08-464-517-19	US-08-464-51/-20 US-08-246-361A-19	US-08-246-361A-20	US-08-463-772-20	US-08-460-744-2	US-07-667-711B-2	US-08-947-492-8	PCT-US93-05000-2	PCT-US93-05000-19	PCT-US93-05000-20	US-08-464-517-4	US-08-463-772-4	US-08-770-761A-3	US-08-770-761A-8
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## ALIGNMENTS

US-08-637-759B-236  US-08-637-759B-236  Sequence 236, Application US/08637759B  Patent No. 5876331  GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: Identification on UNDER OF SEQUENCES: 501 CORRESPONDENCE ADDRESS: ADDRESSEE: Patrea L. Pabst STREET: 1201 West Peachtree Street CITY: Atlanta STREET: 1201 West Peachtree Street CITY: Atlanta STREET: 1201 West Peachtree Street CITY: Atlanta STREET: 1201 West Peachtree Street CITY: Atlanta STREET: 200 One Atlantic Center STREET: 30309-3450 COUNTRY: USA ZIP: 30309-3450 COMPUTER READABLE FORM: MEDIUM TYPE: PLOEDY MISSER: US/08/08-DOS SOFTWARE: Patentin Release #1.0, VCURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/637,759B FILING DATE: 03-MAY-1996 CLASSIFICATION: 435 FRIGN APPLICATION: 435 FRIGN APPLICATION: WAS: 11-DEC-1995 CLASSIFICATION: WAS: 11-DEC-1995 CLASSIFICATION: WAS: 11-DEC-1995 TELEPHONE: 1435 ATTORNEY AGRAT INFORMATION: TELEPHONE: (404) 873-8795 INFORMATION FOR SEQ ID NO: 236: SEQUENCE CHARACTERISTICS: LENGTH: 45 amino acid STREE: STRUES: Single
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audet-909-4.rai

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Georgia
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STATE: Te
COUNTRY:
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/875
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: PELING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: RPMS 101 CON
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TELESSIFICATION NUMBER: RPMS 101 CON
TELESCOMMUNICATION NUMBER: RPMS 101 CON
TELECOMMUNICATION NUMBER: RPMS
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US-09-201-945-236
; Sequence 236, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                             Sequence 236, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 45 amino acids
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Best Local Similarity 60.0°
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STRANDEDNESS: single
EEVVPVGMSY 10
                                         ||: |:| ||
EEISPLGWSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPVGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-871-355A-236
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Wid-08-580-988A-23

Sequence 23, Application US/08580988A

Sequence 23, Application US/08580988A

Sequence 23, Application US/0858098BA

Sequence 23, Application US/0858098BA

Sequence 23, Application US/0858098BA

Tarent Now Invertion:

TITLE OF INVENTION: Properties Fractor

TITLE OF INVENTION: Properties Section Kinase And Methods

TITLE OF INVENTION: Properties Section Contractor Number OF Sequences: 27

CORRESPONDENCE ADDRESS:

ADDRESSE: Dr. Benjamin A. Adler

STREET: 8011 Candle Lane

CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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Pred. No. 3.6;
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                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benjamin Aaron Adler, Ph.D., J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PADSE, PATTOR L.
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (404) 873-8794
TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.6
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEISPLGWSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
30309-3450
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20 EEVFPLAMNY 29

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0; Gaps
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Pred. No. 23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                          61.8%; Score 34; DB 2; Length 102; 60.0%; Pred. No. 14; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD! Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-UNN-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:

NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
  35,423
ER: D5721CIP2
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D572
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-2321
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.8%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                           LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                       no
PR: internal
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 EEVFPLAMINY 33
                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                  US-08-580-988A-23
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US-08-460-694-4
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1 EEVVPVGMSY 10

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Gaps
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0
                                 Sequence 4, Application US/08460744

Patent No. 6107541

GENERAL INFORMATION:

APPLICANT: Arnold, Andrew

TITLE OF INVENTION: PRADI Cyclin and its CDNA

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.8%; Score 34; DB 3; Length 152; Best Local Similarity 60.0%; Pred. No. 23; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INFORMATION: Pradi Cyclin and Its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: MASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILLING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIF: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 EEVFPLAMNY 29
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STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                             20002
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                                                                                                                                                                                                                                                                                                       COUNTRY:
RESULT 6
US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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Gaps ; 0

2; Indels

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Pred. No. 27;
2; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
   Best Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 189 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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Best Local Similarity 60.0
Matches 6; Conservative
                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-464-517-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPVGMSY 10
                                                                                               1 EEVVPVGMSY 10
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                                                                                                                                                            55 EEVFPLAMNY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                    US-08-464-517-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: M. COUNTRY:
                                 Matches
                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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APPLICANT: WEBSTER, KEVIN G.
TITLE OF INVENTION: PEPTIDE INLIGHTORS OF THE P33CDK2 AND
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.8%; Score 34; DB 3; Length 152; Best Local Similarity 60.0%; Pred, No. 23; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%; Score 34; DB 1; Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UNLIBD CLAIRS
ZIF: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER I BEM PC compatible
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
CLASSIFICATION NUMBER: 33.208
TLASSIFICATION NUMBER: 33.208
REFERENCE/DOCKET NUMBER: 5998-0016
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION OF 77.3231
INFORMATION FOR SEQ ID NO: 77.
SEQUENCE CHARACTERISTICS:
FEMILE THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECOMMUTICATION OF THE TELECO
                    APPLICATION DATE:

APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
ACTASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REGISTRATION NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
TELEFANE: (202) 371-2600
TELEFANE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GIARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: REED & ROBINS
1: 615 BRYANT STREET
PALO ALTO
CALIFORNIA
(Y: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08193977
Patent No. 5625031
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: not relevant; MOLECULE TYPE: peptide US-07-667-711B-4
   CURRENT APPLICATION DATA:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EEVFPLAMNY 29
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US-08-193-977-7
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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RESULT 10

US-08-246-361A-21
; Sequence 21, Application US/08246361A
; Sequence 21, 599582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
Sequence 21, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%; Score 34; DB 2; Length 189; 60.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 057/963,308
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
PRILING DATE: 16-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTATION NUMBER: 36,709
REFERENCE DOCKET NUMBER: MI-004C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 157.7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 21:
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COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY.1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: DECURNORMING ACID
TYPE: DECURNORMING ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
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MOLECULE TYPE: peptide

US-08-463-772-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US93-05000-21
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| Sequence 21, Application US/08463772
| Patent No. 6066501
| Patent No. 6066501
| APPLICANT: BEACH, David H. APPLICANT: BEACH, David H. APPLICANT: BEACH, David H. APPLICANT: BEACH, David H. APPLICANT: BEACHLORS: 50
| CORRESPONDENCE ADDRESS: 50
| CORRESPONDENCE ADDRESS: 50
| CORRESPONDENCE ADDRESS: 50
| CONTRY: USA STATE: MA
| COUNTRY: USA STATE: MA
| COUNTRY: USA STATE: PAPPLY (SA) STATE: MADDRES Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.8%; Score 34; DB 2; Length 189; 60.0%; Pred. No. 29; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                        OPERATING SYSTEM: E-LUGS/M3-LUGS
SOCTAMER: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION NUMBER: US O7/963,308
FILING DATE: 16-CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US O7/988,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US O7/88,178
FILING DATE: 26-MAY-1991
ATTORNEY/AGBNT INFORMATION:
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MI-004C
TELECPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTER/STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                               COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: ASCII(tevt)
                     E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 189 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0'
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-246-361A-21
                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
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STREET: 60
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                     ADDRESSEE:
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Sequence 21, Application PC/TUS9305000

Sequence 21, Application PC/TUS9305000

RENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
COUNTRY: US
COUNTRY: US
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CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/963,308
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CCT-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/701,514
APPLICATION NUMBER: US 07/701,514
ATTORNEY AGENT INFORMATION:
NAME: MATCHEW P. Vincent
REGISTRATION NUMBER: 36,709
REBERNEC/CONCET NUMBER: 36,709
RESISTRATION NUMBER: 36,709
RESISTRATION NUMBER: 36,709
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH 1.189 aming acids
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audet-909-4.rai

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2; Mismatches
                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION NUMBER: US 07/963,108
FILING DATE: 16-OCT-1992
PRIOR APPLICATION NUMBER: US 07/963,108
FILING DATE: 16-OCT-1991
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/SOCKET NUMBER: 36,709
REFERENCE/SOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 22:
SEQUENCE SEQ ID NO: 22:
SEQUENCE SEQ ID NO: 22:
SEQUENCE SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY SECOND SIGNEY 
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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                                                                                                                                                                       STATE: MA
COUNTRY: USA
02109
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Patent No. 5869640
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDING ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                      Score 34; DB 5; Length 189;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.8%; Score 34; DB 2; Length 236; 60.0%; Pred. No. 38;
                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/889,178
FILING DATE: 16-MAX-1991
ATTORNEY/AGBNT INFORMATION:
NAME: MALCHAW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-246-361A-22
Sequence 22, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 236 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0°
                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-464-517-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| |: |:|
20 EEVFPLAMNY 29
                                                                                                                                                              1 EEVVPVGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 60 Sta
CITY: Boston
STATE: MA
PCT-US93-05000-21
                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-464-517-22
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Sequence 22, Application US/08463772

Sequence 22, Application US/08463772

PAUGHT NO. 606501

GENERAL INFORMATION:

APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSE: ADDRESS:

STREET: 60 State Street
APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
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Pred. No. 38;
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